

SEQUENCE LISTING

<110> Wonderling, Ramani S.
Boroughs, Karen L.

<120> CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
THEREOF

<130> IM-5

<140> 09/917,265
<141> 2001-07-27

<150> 60/223,016
<151> 2000-08-04

<160> 111

<170> PatentIn version 3.2

<210> 1
<211> 514
<212> DNA
<213> Felis catus

<220>
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<222> (114)..(512)

<220>
<221> misc_feature
<222> (470)..(470)
<223> n = unknown at position 470
Xaa = unknown at position 119

<400> 1
gctaaaggcg ctccgtccac cttctgccat ctacacagct cagaaaaaga aaggacctc 60

aaaccttcca gatcccttcc tctcttagga aactatttag cacagggata aag atg 116
Met
1

act gct ata cca gta gat gat tgc atc aac ttt gtg gga atg aaa ttt 164
Thr Ala Ile Pro Val Asp Asp Cys Ile Asn Phe Val Gly Met Lys Phe
5 10 15

att gac aat aca ctt tac ttt gta gct gac agt gat gaa aac ctg gaa 212
Ile Asp Asn Thr Leu Tyr Phe Val Ala Asp Ser Asp Glu Asn Leu Glu
20 25 30

aca gat tac ttt ggc aag ctt gaa cat aaa ctc tca atc tta cga aac 260
Thr Asp Tyr Phe Gly Lys Leu Glu His Lys Leu Ser Ile Leu Arg Asn
35 40 45

ttg aac gac caa gtt ctc ttc att aac cag gga gat caa cct gtg ttt 308
Leu Asn Asp Gln Val Leu Phe Ile Asn Gln Gly Asp Gln Pro Val Phe

50	55	60	65	
gag gat atg cct gat tct gac tgt aca gat aat gca ccc cgg act gaa Glu Asp Met Pro Asp Ser Asp Cys Thr Asp Asn Ala Pro Arg Thr Glu				356
70	75	80		
ttt atc ata tat atg tat aaa gat agc ctc act aga ggt ctg gca gta Phe Ile Ile Tyr Met Tyr Lys Asp Ser Leu Thr Arg Gly Leu Ala Val				404
85	90	95		
acc atc tct gtg aat tat aag acc atg tct act ctc tcc tgt gag aac Thr Ile Ser Val Asn Tyr Lys Thr Met Ser Thr Leu Ser Cys Glu Asn				452
100	105	110		
aaa att att tcc ttt aan gga atg agt cct cct gag agt atc aat gat Lys Ile Ile Ser Phe Xaa Gly Met Ser Pro Pro Glu Ser Ile Asn Asp				500
115	120	125		
gaa gga aat gac at Glu Gly Asn Asp				514
130				
<210> 2				
<211> 133				
<212> PRT				
<213> Felis catus				
<220>				
<221> misc_feature				
<222> (119)..(119)				
<223> The 'Xaa' at location 119 stands for Lys, or Asn.				
<400> 2				
Met Thr Ala Ile Pro Val Asp Asp Cys Ile Asn Phe Val Gly Met Lys 1 5 10 15				
Phe Ile Asp Asn Thr Leu Tyr Phe Val Ala Asp Ser Asp Glu Asn Leu 20 25 30				
Glu Thr Asp Tyr Phe Gly Lys Leu Glu His Lys Leu Ser Ile Leu Arg 35 40 45				
Asn Leu Asn Asp Gln Val Leu Phe Ile Asn Gln Gly Asp Gln Pro Val 50 55 60				
Phe Glu Asp Met Pro Asp Ser Asp Cys Thr Asp Asn Ala Pro Arg Thr 65 70 75 80				
Glu Phe Ile Ile Tyr Met Tyr Lys Asp Ser Leu Thr Arg Gly Leu Ala 85 90 95				

Val Thr Ile Ser Val Asn Tyr Lys Thr Met Ser Thr Leu Ser Cys Glu
100 105 110

Asn Lys Ile Ile Ser Phe Xaa Gly Met Ser Pro Pro Glu Ser Ile Asn
115 120 125

Asp Glu Gly Asn Asp
130

<210> 3
<211> 514
<212> DNA
<213> Felis catus

<220>
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<222> (45)..(45)
<223> n = unknown at position 45

<400> 3
atgtcatttc cttcatcatt gatactctca ggaggactca ttccnttaaa ggaaataatt 60
ttgttctcac aggagagagt agacatggtc ttataattca cagagatggt tactgccaga 120
cctctagtga ggctatctt atacatatat atgataaatt cagtcgggg tgcattatct 180
gtacagtcag aatcagggcat atcctcaaac acaggttgat ctccctgggt aatgaagaga 240
acttggtcgt tcaagttcg taagatttag agtttatgtt caagcttgcc aaagtaatct 300
gtttccaggt tttcatcact gtcagctaca aagtaaagtg tattgtcaat aaatttcatt 360
cccacaaaagt tcatgcatac atctactggt atagcagtca tctttatccc tgtgctcaat 420
agtttcctaa gagaggaagg gatctggaag gtttgaggtc ctttctttt cctgagctgt 480
gttagatggca gaaggtggca ggagcgccctt tagc 514

<210> 4
<211> 502
<212> DNA
<213> Felis catus

<220>
<221> CDS
<222> (3)..(464)

<220>
<221> misc_feature

<222> (126)..(126)

<223> n = unknown at position 126

Xaa = unknown at position 42

<400> 4

gc aag ctt gaa cat aaa ctc tca atc tta cga aac ttg aac gac caa 47
 Lys Leu Glu His Lys Leu Ser Ile Leu Arg Asn Leu Asn Asp Gln
 1 5 10 15

gtt ctc ttc att aac cag gga gat caa cct gtg ttt gag gag atg cct 95
 Val Leu Phe Ile Asn Gln Gly Asp Gln Pro Val Phe Glu Asp Met Pro
 20 25 30

gat tct gac tgt aca gat aat gca ccc cg_g nct gaa ttt atc ata tat 143
 Asp Ser Asp Cys Thr Asp Asn Ala Pro Arg Xaa Glu Phe Ile Ile Tyr
 35 40 45

atg tat aaa gat agc ctc act aga ggt ctg gca gta acc atc tct gtg 191
Met Tyr Lys Asp Ser Leu Thr Arg Gly Leu Ala Val Thr Ile Ser Val
50 55 60

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aat tat aag acc atg tct act ctc tcc tgt gag aac aaa att att tcc      239
Asn Tyr Lys Thr Met Ser Thr Leu Ser Cys Glu Asn Lys Ile Ile Ser
65          70          75

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ttt aag gaa atg agt cct cct gag agt atc aat gat gaa gga aat gac 287
Phe Lys Glu Met Ser Pro Pro Glu Ser Ile Asn Asp Glu Gly Asn Asp
80 85 90 95

atc ata ttc ttt cag aga agt gtt cca gga cat gat gat aag ata caa
 Ile Ile Phe Phe Gln Arg Ser Val Pro Gly His Asp Asp Lys Ile Gln
 100 105 110

ttt gag tct tca ttg tac aag ggg tac ttt cta gct tgt gaa aaa gag 383
Phe Glu Ser Ser Leu Tyr Lys Gly Tyr Phe Leu Ala Cys Glu Lys Glu
115 120 125

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aaa gat ctt ttc aaa ctc att ttg aaa aaa aag gat gaa aat ggg gat      431
Lys Asp Leu Phe Lys Leu Ile Leu Lys Lys Lys Asp Glu Asn Gly Asp
          130           135           140

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aag tcc ata atg ttc act gtt caa aac aag aat tagatattaa aattgcataa 484
Lys Ser Ile Met Phe Thr Val Gln Asn Lys Asn
145 150

tttggaaaaaa aaaaaaaaaa

<210> 5

<210> 3

<211> 134
<212> BBT

<212> PRI

2203

<220>

<221> MISC_

<222> The !Xaa! at location 42 stands for Thr, Ala, Pro or Ser

<400> 5

Lys Leu Glu His Lys Leu Ser Ile Leu Arg Asn Leu Asn Asp Gln Val
1 5 10 15

Leu Phe Ile Asn Gln Gly Asp Gln Pro Val Phe Glu Asp Met Pro Asp
20 25 30

Ser Asp Cys Thr Asp Asn Ala Pro Arg Xaa Glu Phe Ile Ile Tyr Met
35 40 45

Tyr Lys Asp Ser Leu Thr Arg Gly Leu Ala Val Thr Ile Ser Val Asn
50 55 60

Tyr Lys Thr Met Ser Thr Leu Ser Cys Glu Asn Lys Ile Ile Ser Phe
65 70 75 80

Lys Glu Met Ser Pro Pro Glu Ser Ile Asn Asp Glu Gly Asn Asp Ile
85 90 95

Ile Phe Phe Gln Arg Ser Val Pro Gly His Asp Asp Lys Ile Gln Phe
100 105 110

Glu Ser Ser Leu Tyr Lys Gly Tyr Phe Leu Ala Cys Glu Lys Glu Lys
115 120 125

Asp Leu Phe Lys Leu Ile Leu Lys Lys Asp Glu Asn Gly Asp Lys
130 135 140

Ser Ile Met Phe Thr Val Gln Asn Lys Asn
145 150

<210> 6
<211> 502
<212> DNA
<213> Felis catus

<220>
<221> misc_feature
<222> (377)..(377)
<223> n = unknown at position 377

<400> 6
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attatggact tatccccatt ttcatcctt ttttcaaaa tgagttgaa aagatcttc	120
tcttttcac aagctagaaa gtaccccttg tacaatgaag actcaaattg tatcttatca	180
tcatgtcctg gaacacttct ctgaaaagaat atgatgtcat ttccttcata attgatactc	240
tcaggaggac tcatttcctt aaaggaaata attttggctcacaggagag agtagacatg	300
gtcttataat tcacagagat ggttactgcc agacctctg tgaggctatc tttatacata	360
tatatgataa attcagnccg ggggcattatctgtacagt cagaatcagg catatcctca	420
aacacagggtt gatctccctg gttaatgaag agaacttggt cgttcaagtt tcgtaagatt	480
gagagtttat gttcaagctt gc	502

<210> 7
<211> 607
<212> DNA
<213> Felis catus

<220>	
<221> CDS	
<222> (24) .. (599)	
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Met Thr Ala Ile Pro Val Asp Asp Cys Ile	
1 5 10	
aac ttt gtg gga atg aaa ttt att gac aat aca ctt tac ttt gta gct	101
Asn Phe Val Gly Met Lys Phe Ile Asp Asn Thr Leu Tyr Phe Val Ala	
15 20 25	
gac agt gat gaa aac ctg gaa aca gat tac ttt ggc aag ctt gaa cat	149
Asp Ser Asp Glu Asn Leu Glu Thr Asp Tyr Phe Gly Lys Leu Glu His	
30 35 40	
aaa ctc tca atc tta cga aac ttg aac gac caa gtt ctc ttc att aac	197
Lys Leu Ser Ile Leu Arg Asn Leu Asn Asp Gln Val Leu Phe Ile Asn	
45 50 55	
cag gga gat caa cct gtg ttt gag gat atg cct gat tct gac tgt aca	245
Gln Gly Asp Gln Pro Val Phe Glu Asp Met Pro Asp Ser Asp Cys Thr	
60 65 70	
gat aat gca ccc cgg act gaa ttt atc ata tat atg tat aaa gat agc	293
Asp Asn Ala Pro Arg Thr Glu Phe Ile Ile Tyr Met Tyr Lys Asp Ser	
75 80 85 90	
ctc act aga ggt ctg gca gta acc atc tct gtg aat tat aag acc atg	341
Leu Thr Arg Gly Leu Ala Val Thr Ile Ser Val Asn Tyr Lys Thr Met	
95 100 105	
tct act ctc tcc tgt gag aac aaa att att tcc ttt aag gaa atg agt	389

Ser Thr Leu Ser Cys Glu Asn Lys Ile Ile Ser Phe Lys Glu Met Ser			
110	115	120	
cct cct gag agt atc aat gat gaa gga aat gac atc ata ttc ttt cag			437
Pro Pro Glu Ser Ile Asn Asp Glu Gly Asn Asp Ile Ile Phe Phe Gln			
125	130	135	
aga agt gtt cca gga cat gat gat aag ata caa ttt gag tct tca ttg			485
Arg Ser Val Pro Gly His Asp Asp Lys Ile Gln Phe Glu Ser Ser Leu			
140	145	150	
tac aag ggg tac ttt cta gct tgt gaa aaa gag aaa gat ctt ttc aaa			533
Tyr Lys Gly Tyr Phe Leu Ala Cys Glu Lys Glu Lys Asp Leu Phe Lys			
155	160	165	170
ctc att ttg aaa aaa aag gat gaa aat ggg gat aag tcc ata atg ttc			581
Leu Ile Leu Lys Lys Asp Glu Asn Gly Asp Lys Ser Ile Met Phe			
175	180	185	
act gtt caa aac aag aat tagatatt			607
Thr Val Gln Asn Lys Asn			
190			
<210> 8			
<211> 192			
<212> PRT			
<213> Felis catus			
<400> 8			
Met Thr Ala Ile Pro Val Asp Asp Cys Ile Asn Phe Val Gly Met Lys			
1	5	10	15
Phe Ile Asp Asn Thr Leu Tyr Phe Val Ala Asp Ser Asp Glu Asn Leu			
20	25	30	
Glu Thr Asp Tyr Phe Gly Lys Leu Glu His Lys Leu Ser Ile Leu Arg			
35	40	45	
Asn Leu Asn Asp Gln Val Leu Phe Ile Asn Gln Gly Asp Gln Pro Val			
50	55	60	
Phe Glu Asp Met Pro Asp Ser Asp Cys Thr Asp Asn Ala Pro Arg Thr			
65	70	75	80
Glu Phe Ile Ile Tyr Met Tyr Lys Asp Ser Leu Thr Arg Gly Leu Ala			
85	90	95	
Val Thr Ile Ser Val Asn Tyr Lys Thr Met Ser Thr Leu Ser Cys Glu			
100	105	110	

Asn Lys Ile Ile Ser Phe Lys Glu Met Ser Pro Pro Glu Ser Ile Asn
115 120 125

Asp Glu Gly Asn Asp Ile Ile Phe Phe Gln Arg Ser Val Pro Gly His
130 135 140

Asp Asp Lys Ile Gln Phe Glu Ser Ser Leu Tyr Lys Gly Tyr Phe Leu
145 150 155 160

Ala Cys Glu Lys Glu Lys Asp Leu Phe Lys Leu Ile Leu Lys Lys Lys
165 170 175

Asp Glu Asn Gly Asp Lys Ser Ile Met Phe Thr Val Gln Asn Lys Asn
180 185 190

<210> 9

<211> 576

<212> DNA

<213> Felis catus

<400> 9

atgactgcta taccagtaga tgattgcata aactttgtgg gaatgaaatt tattgacaat 60

acactttact ttgttagctga cagtgtgaa aacctggaaa cagattactt tggcaagctt 120

gaacataaac tctcaatctt acgaaacttg aacgaccaag ttctcttcat taaccaggga 180

gatcaacctg tgtttgagga tatgcctgat tctgactgta cagataatgc accccggact 240

gaatttatca tatatatgtt aaaagatagc ctcactagag gtctggcagt aaccatctct 300

gtgaattata agaccatgtc tactctctcc tgtgagaaca aaattatttc cttaaggaa 360

atgagtcctc ctgagagttt caatgtgaa gaaaaatgaca tcattttctt tcagagaagt 420

gttccaggac atgatgataa gatacaattt gagtcttcat tgtacaaggg gtactttcta 480

gcttgtgaaa aagagaaaga tctttcaaa ctcattttga aaaaaaagga tgaaaatggg 540

gataagtcca taatgttcac tggcaaaac aagaat 576

<210> 10

<211> 607

<212> DNA

<213> Felis catus

<400> 10

aatatctaat tcttggtttt aacagtgaac attatggact tatccccatt ttcatttc 60

ttttcaaaa tgagttgaa aagatcttc tctttcac aagctagaaa gtacccctt	120
tacaatgaag actcaaattg tatcttatca tcacgtcctg gaacacttct ctgaaagaat	180
atgatgtcat ttccatcattgatactc tcaggaggac tcatttcctt aaaggaaata	240
atttgttct cacaggagag agtagacatg gtcttataat tcacagagat ggtaactgcc	300
agacctctag tgaggctatc ttatatacata tatatgataa attcagtccg ggggcattt	360
tctgtacagt cagaatcagg catatcctca aacacagggtt gatctccctg gttaatgaag	420
agaacttggt cggtcaagtt tcgtaagatt gagagttt gttcaagctt gccaaagtaa	480
tctgtttcca ggtttcatc actgtcagct acaaagtaaa gtgtattgtc aataaatttc	540
atccccacaa agttgatgca atcatctact ggtatagcag tcatcttatt ccctgtgctc	600
aatagtt	607

<210> 11
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<212> DNA
<213> Felis catus

<220>	
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Tyr Phe Gly Lys Leu Glu His Lys Leu Ser Ile Leu Arg Asn Leu Asn	
1 5 10 15	
gac caa gtt ctc ttc att aac cag gga gat caa cct gtg ttt gag gat	96
Asp Gln Val Leu Phe Ile Asn Gln Gly Asp Gln Pro Val Phe Glu Asp	
20 25 30	
atg cct gat tct gac tgt aca gat aat gca ccc cgg act gaa ttt atc	144
Met Pro Asp Ser Asp Cys Thr Asp Asn Ala Pro Arg Thr Glu Phe Ile	
35 40 45	
ata tat atg tat aaa gat agc ctc act aga ggt ctg gca gta acc atc	192
Ile Tyr Met Tyr Lys Asp Ser Leu Thr Arg Gly Leu Ala Val Thr Ile	
50 55 60	
tct gtg aat tat aag acc atg tct act ctc tcc tgt gag aac aaa att	240
Ser Val Asn Tyr Lys Thr Met Ser Thr Leu Ser Cys Glu Asn Lys Ile	
65 70 75 80	
att tcc ttt aag gaa atg agt cct gag agt atc aat gat gaa gga	288
Ile Ser Phe Lys Glu Met Ser Pro Pro Glu Ser Ile Asn Asp Glu Gly	
85 90 95	
aat gac atc ata ttc ttt cag aga agt gtt cca gga cat gat gat aag	336

Asn Asp Ile Ile Phe Phe Gln Arg Ser Val Pro Gly His Asp Asp Lys			
100	105	110	
ata caa ttt gag tct tca ttg tac aag ggg tac ttt cta gct tgt gaa			384
Ile Gln Phe Glu Ser Ser Leu Tyr Lys Gly Tyr Phe Leu Ala Cys Glu			
115	120	125	
aaa gag aaa gat ctt ttc aaa ctc att ttg aaa aaa aag gat gaa aat			432
Lys Glu Lys Asp Leu Phe Lys Leu Ile Leu Lys Lys Asp Glu Asn			
130	135	140	
ggg gat aag tcc ata atg ttc act gtt caa aac aag aat			471
Gly Asp Lys Ser Ile Met Phe Thr Val Gln Asn Lys Asn			
145	150	155	
<210> 12			
<211> 157			
<212> PRT			
<213> Felis catus			
<400> 12			
Tyr Phe Gly Lys Leu Glu His Lys Leu Ser Ile Leu Arg Asn Leu Asn			
1	5	10	15
Asp Gln Val Leu Phe Ile Asn Gln Gly Asp Gln Pro Val Phe Glu Asp			
20	25	30	
Met Pro Asp Ser Asp Cys Thr Asp Asn Ala Pro Arg Thr Glu Phe Ile			
35	40	45	
Ile Tyr Met Tyr Lys Asp Ser Leu Thr Arg Gly Leu Ala Val Thr Ile			
50	55	60	
Ser Val Asn Tyr Lys Thr Met Ser Thr Leu Ser Cys Glu Asn Lys Ile			
65	70	75	80
Ile Ser Phe Lys Glu Met Ser Pro Pro Glu Ser Ile Asn Asp Glu Gly			
85	90	95	
Asn Asp Ile Ile Phe Phe Gln Arg Ser Val Pro Gly His Asp Asp Lys			
100	105	110	
Ile Gln Phe Glu Ser Ser Leu Tyr Lys Gly Tyr Phe Leu Ala Cys Glu			
115	120	125	
Lys Glu Lys Asp Leu Phe Lys Leu Ile Leu Lys Lys Asp Glu Asn			
130	135	140	

Gly Asp Lys Ser Ile Met Phe Thr Val Gln Asn Lys Asn
145 150 155

<210> 13
<211> 471
<212> DNA
<213> *Felis catus*

<400> 13 attcttgaaa tgaacagtga acattatgga cttatccccca ttttcatcct tttttttcaa 60
aatgagtttggaaa aaaaatctt tctcttttc acaagctaga aagtacccct tgtacaatga 120
agactcaaataat tgtatcttat catcatgtcc tggaacactt ctctgaaaga atatgatgtc 180
atttccttca tcattgatac tctcaggagg actcatttcc ttaaaggaaa taattttgtt 240
ctcacaggag agagtagaca tggtcttata attcacagag atggttactg ccagacctct 300
agtggaggcta tctttataca tatatatgat aaattcagtc cggggtgcat tatctgtaca 360
gtcagaatca ggcataatcct caaacacagg ttgatctccc tggtaatga agagaacttg 420
gtcggttcaag ttgcgttggaaa ttgagatgtt atgttcaagc ttgcggaaatgtt a 471

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<210> 14
<211> 1233
<212> DNA
<213> Felis catus
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<220>
<221> CDS
<222> (1) .. (1230)

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65	70	75	80
acc cac ctt gca gag acg ctg ggg ctc tcc tca agc cca caa tct gga			288
Thr His Leu Ala Glu Thr Leu Gly Leu Ser Ser Ser Pro Gln Ser Gly			
85	90	95	
aat tct cag aac acc acg gac tct gaa gta gcg ttt cct cct ctt cca			336
Asn Ser Gln Asn Thr Thr Asp Ser Glu Val Ala Phe Pro Pro Leu Pro			
100	105	110	
gcc agc gtg aat aac atg cct ggg ccg gct gag cca gaa gaa tct gta			384
Ala Ser Val Asn Asn Met Pro Gly Pro Ala Glu Pro Glu Glu Ser Val			
115	120	125	
gat gct ctc aag ctt tgt cct cgt gaa aac ttc gtg aaa ctg tgt aaa			432
Asp Ala Leu Lys Leu Cys Pro Arg Glu Asn Phe Val Lys Leu Cys Lys			
130	135	140	
cag agg gct gaa gag atc tac cca ata aag gag aga aag gat cgt act			480
Gln Arg Ala Glu Glu Ile Tyr Pro Ile Lys Glu Arg Lys Asp Arg Thr			
145	150	155	160
cgt ctg gct ctc atc ata tgc aat acg acg ttc gat cat ctt tct ctc			528
Arg Leu Ala Leu Ile Ile Cys Asn Thr Thr Phe Asp His Leu Ser Leu			
165	170	175	
agg aag ggg gct gac ctt gac gtt gca ggg atg agg agg ctg ctt aca			576
Arg Lys Gly Ala Asp Leu Asp Val Ala Gly Met Arg Arg Leu Leu Thr			
180	185	190	
gac ctt ggc tac agt gtg cac ata aaa gag gaa ctc act gct aag gac			624
Asp Leu Gly Tyr Ser Val His Ile Lys Glu Glu Leu Thr Ala Lys Asp			
195	200	205	
atg gaa tca gag ctg agg gca ttt gct gcc cgt cca gag cac aag tcc			672
Met Glu Ser Glu Leu Arg Ala Phe Ala Ala Arg Pro Glu His Lys Ser			
210	215	220	
tcg gac agc aca ttc ctg gtg ttc atg tct cat ggc atc ctg agt gga			720
Ser Asp Ser Thr Phe Leu Val Phe Met Ser His Gly Ile Leu Ser Gly			
225	230	235	240
atc tgt ggg acg aag tac agc gct gaa gga gac cca gat gta ttg gct			768
Ile Cys Gly Thr Lys Tyr Ser Ala Glu Gly Asp Pro Asp Val Leu Ala			
245	250	255	
tat gac acc atc ttc cag att ttc aac aac cgc aac tgc ctt agt cta			816
Tyr Asp Thr Ile Phe Gln Ile Phe Asn Asn Arg Asn Cys Leu Ser Leu			
260	265	270	
aag gac aag ccc aag gtc atc atc gtc cag gcc tgc aga ggt gaa aat			864
Lys Asp Lys Pro Lys Val Ile Ile Val Gln Ala Cys Arg Gly Glu Asn			
275	280	285	
ttg ggg gaa ctg ttg atc agt gac tct cca gcg gcc cca atg gac agc			912
Leu Gly Glu Leu Leu Ile Ser Asp Ser Pro Ala Ala Pro Met Asp Ser			

290	295	300	
act tca cag atg ggt agc agc ctt tca cag gtg ggt gac aac cta gag Thr Ser Gln Met Gly Ser Ser Leu Ser Gln Val Gly Asp Asn Leu Glu 305 310 315 320			960
gac gac gcc att tac aag gtc cac gtg gag aag gac ttc atc gct ttc Asp Asp Ala Ile Tyr Lys Val His Val Glu Lys Asp Phe Ile Ala Phe 325 330 335			1008
tgc tcc tcg acc cca cat cat gtg tct tgg aga gac gtg aac aag gga Cys Ser Ser Thr Pro His His Val Ser Trp Arg Asp Val Asn Lys Gly 340 345 350			1056
tct ctc ttc att aca caa ctc atc acg tgc ttc caa aag tat tcg tgg Ser Leu Phe Ile Thr Gln Leu Ile Thr Cys Phe Gln Lys Tyr Ser Trp 355 360 365			1104
tgc ttt cat ctg gag gaa gta ttt cg ^g aag gta caa cag tca ttt gaa Cys Phe His Leu Glu Glu Val Phe Arg Lys Val Gln Gln Ser Phe Glu 370 375 380			1152
aaa cca aat gtt aga gcc cag atg ccc acc att gaa cga cta tcc atg Lys Pro Asn Val Arg Ala Gln Met Pro Thr Ile Glu Arg Leu Ser Met 385 390 395 400			1200
aca aga tgt ttc tac ctc ttc cca gga cat taa Thr Arg Cys Phe Tyr Leu Phe Pro Gly His 405 410			1233
<210> 15			
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<212> PRT			
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<400> 15			
Met Ala Asp Lys Val Leu Lys Glu Lys Arg Lys Gln Phe Ile Asn Ser 1 5 10 15			
Val Gly Met Gly Thr Val Asn Gly Leu Leu Asp Glu Leu Phe Glu Lys 20 25 30			
Asn Val Leu Asn Gln Glu Glu Met Glu Arg Val Lys Cys Glu Asn Ala 35 40 45			
Thr Val Met Asp Lys Ala Arg Ala Leu Ile Asp Ser Val Leu Arg Lys 50 55 60			
Gly Pro Arg Ala Cys Gln Ile Phe Ile Cys His Ile Cys Glu Glu Asp 65 70 75 80			

Thr His Leu Ala Glu Thr Leu Gly Leu Ser Ser Ser Pro Gln Ser Gly		
85	90	95
Asn Ser Gln Asn Thr Thr Asp Ser Glu Val Ala Phe Pro Pro Leu Pro		
100	105	110
Ala Ser Val Asn Asn Met Pro Gly Pro Ala Glu Pro Glu Glu Ser Val		
115	120	125
Asp Ala Leu Lys Leu Cys Pro Arg Glu Asn Phe Val Lys Leu Cys Lys		
130	135	140
Gln Arg Ala Glu Glu Ile Tyr Pro Ile Lys Glu Arg Lys Asp Arg Thr		
145	150	155
160		
Arg Leu Ala Leu Ile Ile Cys Asn Thr Thr Phe Asp His Leu Ser Leu		
165	170	175
Arg Lys Gly Ala Asp Leu Asp Val Ala Gly Met Arg Arg Leu Leu Thr		
180	185	190
Asp Leu Gly Tyr Ser Val His Ile Lys Glu Glu Leu Thr Ala Lys Asp		
195	200	205
Met Glu Ser Glu Leu Arg Ala Phe Ala Ala Arg Pro Glu His Lys Ser		
210	215	220
Ser Asp Ser Thr Phe Leu Val Phe Met Ser His Gly Ile Leu Ser Gly		
225	230	235
240		
Ile Cys Gly Thr Lys Tyr Ser Ala Glu Gly Asp Pro Asp Val Leu Ala		
245	250	255
Tyr Asp Thr Ile Phe Gln Ile Phe Asn Asn Arg Asn Cys Leu Ser Leu		
260	265	270
Lys Asp Lys Pro Lys Val Ile Ile Val Gln Ala Cys Arg Gly Glu Asn		
275	280	285
Leu Gly Glu Leu Leu Ile Ser Asp Ser Pro Ala Ala Pro Met Asp Ser		
290	295	300

Thr Ser Gln Met Gly Ser Ser Leu Ser Gln Val Gly Asp Asn Leu Glu
305 310 315 320

Asp Asp Ala Ile Tyr Lys Val His Val Glu Lys Asp Phe Ile Ala Phe
325 330 335

Cys Ser Ser Thr Pro His His Val Ser Trp Arg Asp Val Asn Lys Gly
340 345 350

Ser Leu Phe Ile Thr Gln Leu Ile Thr Cys Phe Gln Lys Tyr Ser Trp
355 360 365

Cys Phe His Leu Glu Glu Val Phe Arg Lys Val Gln Gln Ser Phe Glu
370 375 380

Lys Pro Asn Val Arg Ala Gln Met Pro Thr Ile Glu Arg Leu Ser Met
385 390 395 400

Thr Arg Cys Phe Tyr Leu Phe Pro Gly His
405 410

<210> 16
<211> 1233
<212> DNA
<213> Felis catus

<400> 16
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atgaaaaggcac cacgaataact tttggaaagca cgtgatgagt tgtgtaatga agagagatcc 180
cttgttcacg tctctccaag acacatgatg tggggtcgag gagcagaaaag cgatgaagtc 240
cttctccacg tggaccttgc aaatggcgtc gtcctctagg ttgtcacccca cctgtgaaag 300
gctgctaccc atctgtgaag tgctgtccat tggggccgct ggagagtcac tgatcaacag 360
ttcccccaaa tttcacctc tgcaggcctg gacgatgatg accttgggct tgccttttag 420
actaaggcag ttgcgggtgt tgaaaatctg gaagatggtg tcataagcca atacatctgg 480
gtctccttca gcgctgtact tcgtcccaca gattccactc aggatgccat gagacatgaa 540
caccaggaat gtgctgtccg aggacttgc ctctggacgg gcagcaaatg ccctcagctc 600
tgattccatg tccttagcag tgagttcctc ttttatgtgc acactgttagc caaggctgt 660
aagcagcctc ctcatccctg caacgtcaag gtcagcccc ttcctgagag aaagatgatc 720

gaacgtcgta ttgcatatga tgagagccag acgagtaga tcctttctct ccttattgg	780
gtagatctct tcagccctct gtttacacag tttcacgaag tttcacgag gacaaagctt	840
gagagcatct acagattctt ctggctcagc cggcccaggc atgttattca cgctggctgg	900
aagaggagga aacgctactt cagagtccgt ggtgttctga gaatttccag attgtggct	960
tgaggagagc cccagcgtct ctgcaaggtg ggtgttcc tcacagatgt gacagataaa	1020
gatctggcac gcccgtggcc ctttccgcag gacgctgtcg atcagagctc gggccttgc	1080
cataacggta gcgtttcac atttactct ctccatctcc tcctgggtca gcacgaaaa	1140
ctcaaagagt tcatccagca agccgttgac cgtccccatg ccgactgagt tgatgaactg	1200
cttcctcttc tccttcagga ccttgcggc cat	1233

<210> 17
<211> 526
<212> DNA
<213> Felis catus

<220>	
<221> CDS	
<222> (18) .. (524)	
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Met Ala Asp Lys Asp Leu Lys Gly Lys Arg Lys	
1 5 10	
cag ttc atc aac tca gtc ggc atg ggg acg gtc aac ggc ttg ctg gat	98
Gln Phe Ile Asn Ser Val Gly Met Gly Thr Val Asn Gly Leu Leu Asp	
15 20 25	
gaa ctc ttt gag aaa aac gtg ctg aac cag gag gag atg gag aga gta	146
Glu Leu Phe Glu Lys Asn Val Leu Asn Gln Glu Glu Met Glu Arg Val	
30 35 40	
aaa tgt gaa aac gct acc gtt atg gac aag gcc cga gct ctg atc gac	194
Lys Cys Glu Asn Ala Thr Val Met Asp Lys Ala Arg Ala Leu Ile Asp	
45 50 55	
agc gtc ctg cgg aaa ggg cca cgg gcg tgc cag atc ttt atc tgt cac	242
Ser Val Leu Arg Lys Gly Pro Arg Ala Cys Gln Ile Phe Ile Cys His	
60 65 70 75	
atc tgt gag gaa gac acc cac ctt gca gag acg ctg ggg ctc tcc tca	290
Ile Cys Glu Asp Thr His Leu Ala Glu Thr Leu Gly Leu Ser Ser	
80 85 90	
agc cca caa tct gga aat tct cag aac acc acg gac tct gaa gta gcg	338
Ser Pro Gln Ser Gly Asn Ser Gln Asn Thr Thr Asp Ser Glu Val Ala	

95	100	105	
ttt cct cct ctt cca gcc agc gtg aat aac atg cct ggg ccg gct gag Phe Pro Pro Leu Pro Ala Ser Val Asn Asn Met Pro Gly Pro Ala Glu 110	115	120	386
cca gaa gaa tct gta gat gct ctc aag ctt tgt cct cgt gaa aac ttc Pro Glu Glu Ser Val Asp Ala Leu Lys Leu Cys Pro Arg Glu Asn Phe 125	130	135	434
gtg aaa ctg tgt aaa cag agg gct gaa gag atc tac cca ata aag gag Val Lys Leu Cys Lys Gln Arg Ala Glu Glu Ile Tyr Pro Ile Lys Glu 140	145	150	482
aga aag gat cgt act cgt ctg gct ctc atc ata tgc aat acg ac Arg Lys Asp Arg Thr Arg Leu Ala Leu Ile Ile Cys Asn Thr 160	165		526
<210> 18			
<211> 169			
<212> PRT			
<213> Felis catus			
<400> 18			
Met Ala Asp Lys Asp Leu Lys Gly Lys Arg Lys Gln Phe Ile Asn Ser 1	5	10	15
Val Gly Met Gly Thr Val Asn Gly Leu Leu Asp Glu Leu Phe Glu Lys 20	25	30	
Asn Val Leu Asn Gln Glu Glu Met Glu Arg Val Lys Cys Glu Asn Ala 35	40	45	
Thr Val Met Asp Lys Ala Arg Ala Leu Ile Asp Ser Val Leu Arg Lys 50	55	60	
Gly Pro Arg Ala Cys Gln Ile Phe Ile Cys His Ile Cys Glu Glu Asp 65	70	75	80
Thr His Leu Ala Glu Thr Leu Gly Leu Ser Ser Ser Pro Gln Ser Gly 85	90	95	
Asn Ser Gln Asn Thr Thr Asp Ser Glu Val Ala Phe Pro Pro Leu Pro 100	105	110	
Ala Ser Val Asn Asn Met Pro Gly Pro Ala Glu Pro Glu Glu Ser Val 115	120	125	

Asp Ala Leu Lys Leu Cys Pro Arg Glu Asn Phe Val Lys Leu Cys Lys
130 135 140

Gln Arg Ala Glu Glu Ile Tyr Pro Ile Lys Glu Arg Lys Asp Arg Thr
145 150 155 160

Arg Leu Ala Leu Ile Ile Cys Asn Thr
165

<210> 19
<211> 526
<212> DNA
<213> Felis catus

<400> 19
gtcgtattgc atatgatgag agccagacga gtacgatcct ttcttcctt tattggtag 60
atctcttcag ccctctgttt acacagttc acgaagttt cacgaggaca aagcttgaga 120
gcacatcacag attcttctgg ctcagccggc ccaggcatgt tattcacgct ggctggaaga 180
ggaggaaacg ctacttcaga gtccgtggtg ttctgagaat ttccagattg tgggcttgag 240
gagagccccca gcgtctctgc aaggtgggtg tcttcctcac agatgtgaca gataaagatc 300
tggcacgccc gtggcccttt ccgcaggacg ctgtcgatca gagctcgggc cttgtccata 360
acgtagcgt tttcacattt tactctctcc atctccctt ggttcagcac gttttctca 420
aagagttcat ccagcaagcc gttgaccgtc cccatgccga ctgagttgat gaactgcttc 480
ctcttgcctt tcagatcctt gtcggccatg gcttttgct cgtgcc 526

<210> 20
<211> 500
<212> DNA
<213> Felis catus

<220>
<221> CDS
<222> (3)..(362)

<220>
<221> misc_feature
<222> (473)..(473)
<223> n = unknown at position 473

<400> 20
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Glu Leu Leu Ile Ser Asp Ser Pro Ala Ala Pro Met Asp Ser Thr
1 5 10 15

tca cag atg ggt agc agc ctt tca cag gtg ggt gac aac cta gag gac Ser Gln Met Gly Ser Ser Leu Ser Gln Val Gly Asp Asn Leu Glu Asp	95
20 25 30	
gac gcc att tac aag gtc cac gtg gag aag gac ttc atc gct ttc tgc Asp Ala Ile Tyr Lys Val His Val Glu Lys Asp Phe Ile Ala Phe Cys	143
35 40 45	
tcc tcg acc cca cat cat gtg tct tgg aga gac gtg aac aag gga tct Ser Ser Thr Pro His His Val Ser Trp Arg Asp Val Asn Lys Gly Ser	191
50 55 60	
ctc ttc att aca caa ctc atc acg tgc ttc caa aag tat tcg tgg tgc Leu Phe Ile Thr Gln Leu Ile Thr Cys Phe Gln Lys Tyr Ser Trp Cys	239
65 70 75	
ttt cat ctg gag gaa gta ttt cgg aag gta caa cag tca ttt gaa aaa Phe His Leu Glu Glu Val Phe Arg Lys Val Gln Gln Ser Phe Glu Lys	287
80 85 90 95	
cca aat gtt aga gcc cag atg ccc acc att gaa cga cta tcc atg aca Pro Asn Val Arg Ala Gln Met Pro Thr Ile Glu Arg Leu Ser Met Thr	335
100 105 110	
aga tac ttc tat ctc ttc cct ggc aat tgaaaatagc aatcatgggc Arg Tyr Phe Tyr Leu Phe Pro Gly Asn	382
115 120	
agtccagccc ttcttgacca acttgaaaaa gtaccttagc tagcacaaca cactcattta	442
acgtttggta tctcaataaa aatgaaaaaca nctaaaaaaaaaaaaaaaaaaaaaaa	500
<210> 21	
<211> 120	
<212> PRT	
<213> Felis catus	
<400> 21	
Glu Leu Leu Ile Ser Asp Ser Pro Ala Ala Pro Met Asp Ser Thr Ser	1
5 10 15	
Gln Met Gly Ser Ser Leu Ser Gln Val Gly Asp Asn Leu Glu Asp Asp	20
25 30	
Ala Ile Tyr Lys Val His Val Glu Lys Asp Phe Ile Ala Phe Cys Ser	35
40 45	
Ser Thr Pro His His Val Ser Trp Arg Asp Val Asn Lys Gly Ser Leu	50
55 60	

Phe Ile Thr Gln Leu Ile Thr Cys Phe Gln Lys Tyr Ser Trp Cys Phe
65 70 75 80

His Leu Glu Glu Val Phe Arg Lys Val Gln Gln Ser Phe Glu Lys Pro
85 90 95

Asn Val Arg Ala Gln Met Pro Thr Ile Glu Arg Leu Ser Met Thr Arg
100 105 110

Tyr Phe Tyr Leu Phe Pro Gly Asn
115 120

<210> 22
<211> 500
<212> DNA
<213> Felis catus

<220>
<221> misc_feature
<222> (28)..(28)
<223> n = unknown at position 28

<400> 22
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aatgagtgtg ttgtgctagc taaggtactt ttccaagttg gtcaagaagg gctggactgc 120
ccatgattgc tattttcaat tgccagggaa gagatagaag tatcttgtca tggatagtcg 180
ttcaatggtg ggcatctggg ctctaacatt tggttttca aatgactgtt gtaccctccg 240
aaatacttcc tccagatgaa agcaccacga atactttgg aagcacgtga tgagttgtgt 300
aatgaagaga gatcccttgt tcacgtctct ccaagacaca tcatgtgggg tcgaggagca 360
gaaagcgatg aagtccttct ccacgtggac cttgtaaatg gcgtcgtcct ctaggttgtc 420
accacacctgt gaaaggctgc tacccatctg tgaagtgctg tccattgggg ccgctggaga 480
gtcactgatc aacagttccc 500

<210> 23
<211> 1230
<212> DNA
<213> Felis catus

<220>
<221> CDS
<222> (1)..(1230)

<400>	23		
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Met Ala Asp Lys Asp Leu Lys Gly Lys Arg Lys Gln Phe Ile Asn Ser			
1	5	10	15
gtc ggc atg ggg acg gtc aac ggc ttg ctg gat gaa ctc ttt gag aaa			96
Val Gly Met Gly Thr Val Asn Gly Leu Leu Asp Glu Leu Phe Glu Lys			
20	25	30	
aac gtg ctg aac cag gag gag atg gag aga gta aaa tgt gaa aac gct			144
Asn Val Leu Asn Gln Glu Met Glu Arg Val Lys Cys Glu Asn Ala			
35	40	45	
acc gtt atg gac aag gcc cga gct ctg atc gac agc gtc ctg cgg aaa			192
Thr Val Met Asp Lys Ala Arg Ala Leu Ile Asp Ser Val Leu Arg Lys			
50	55	60	
ggg cca cgg gcg tgc cag atc ttt atc tgt cac atc tgt gag gaa gac			240
Gly Pro Arg Ala Cys Gln Ile Phe Ile Cys His Ile Cys Glu Glu Asp			
65	70	75	80
acc cac ctt gca gag acg ctg ggg ctc tcc tca agc cca caa tct gga			288
Thr His Leu Ala Glu Thr Leu Gly Leu Ser Ser Pro Gln Ser Gly			
85	90	95	
aat tct cag aac acc acg gac tct gaa gta gcg ttt cct cct ctt cca			336
Asn Ser Gln Asn Thr Asp Ser Glu Val Ala Phe Pro Pro Leu Pro			
100	105	110	
gcc agc gtg aat aac atg cct ggg ccg gct gag cca gaa gaa tct gta			384
Ala Ser Val Asn Asn Met Pro Gly Pro Ala Glu Pro Glu Glu Ser Val			
115	120	125	
gat gct ctc aag ctt tgt cct cgt gaa aac ttc gtg aaa ctg tgt aaa			432
Asp Ala Leu Lys Leu Cys Pro Arg Glu Asn Phe Val Lys Leu Cys Lys			
130	135	140	
cag agg gct gaa gag atc tac cca ata aag gag aga aag gat cgt act			480
Gln Arg Ala Glu Glu Ile Tyr Pro Ile Lys Glu Arg Lys Asp Arg Thr			
145	150	155	160
cgt ctg gct ctc atc ata tgc aat acg acg ttc gat cat ctt tct ctc			528
Arg Leu Ala Leu Ile Ile Cys Asn Thr Thr Phe Asp His Leu Ser Leu			
165	170	175	
agg aag ggg gct gac ctt gac gtt gca ggg atg agg agg ctg ctt aca			576
Arg Lys Gly Ala Asp Leu Asp Val Ala Gly Met Arg Arg Leu Leu Thr			
180	185	190	
gac ctt ggc tac agt gtg cac ata aaa gag gaa ctc act gct aag gac			624
Asp Leu Gly Tyr Ser Val His Ile Lys Glu Glu Leu Thr Ala Lys Asp			
195	200	205	
atg gaa tca gag ctg agg gca ttt gct gcc cgt cca gag cac aag tcc			672
Met Glu Ser Glu Leu Arg Ala Phe Ala Ala Arg Pro Glu His Lys Ser			
210	215	220	

tcg gac agc aca ttc ctg gtg ttc atg tct cat ggc atc ctg agt gga Ser Asp Ser Thr Phe Leu Val Phe Met Ser His Gly Ile Leu Ser Gly 225 230 235 240	720
atc tgt ggg acg aag tac agc gct gaa gga gac cca gat gta ttg gct Ile Cys Gly Thr Lys Tyr Ser Ala Glu Gly Asp Pro Asp Val Leu Ala 245 250 255	768
tat gac acc atc ttc cag att ttc aac aac cgc aac tgc ctt agt cta Tyr Asp Thr Ile Phe Gln Ile Phe Asn Asn Arg Asn Cys Leu Ser Leu 260 265 270	816
aag gac aag ccc aag gtc atc atc gtc cag gcc tgc aga ggt gaa aat Lys Asp Lys Pro Lys Val Ile Ile Val Gln Ala Cys Arg Gly Glu Asn 275 280 285	864
ttg ggg gaa ctg ttg atc agt gac tct cca gcg gcc cca atg gac agc Leu Gly Leu Leu Ile Ser Asp Ser Pro Ala Ala Pro Met Asp Ser 290 295 300	912
act tca cag atg ggt agc agc ctt tca cag gtg ggt gac aac cta gag Thr Ser Gln Met Gly Ser Ser Leu Ser Gln Val Gly Asp Asn Leu Glu 305 310 315 320	960
gac gac gcc att tac aag gtc cac gtg gag aag gac ttc atc gct ttc Asp Asp Ala Ile Tyr Lys Val His Val Glu Lys Asp Phe Ile Ala Phe 325 330 335	1008
tgc tcc tcg acc cca cat cat gtg tct tgg aga gac gtg aac aag gga Cys Ser Ser Thr Pro His His Val Ser Trp Arg Asp Val Asn Lys Gly 340 345 350	1056
tct ctc ttc att aca caa ctc atc acg tgc ttc caa aag tat tcg tgg Ser Leu Phe Ile Thr Gln Leu Ile Thr Cys Phe Gln Lys Tyr Ser Trp 355 360 365	1104
tgc ttt cat ctg gag gaa gta ttt cg ^g aag gta caa cag tca ttt gaa Cys Phe His Leu Glu Glu Val Phe Arg Lys Val Gln Gln Ser Phe Glu 370 375 380	1152
aaa cca aat gtt aga gcc cag atg ccc acc att gaa cga cta tcc atg Lys Pro Asn Val Arg Ala Gln Met Pro Thr Ile Glu Arg Leu Ser Met 385 390 395 400	1200
aca aga tac ttc tat ctc ttc cct ggc aat Thr Arg Tyr Phe Tyr Leu Phe Pro Gly Asn 405 410	1230

<210> 24
<211> 410
<212> PRT
<213> Felis catus

<400> 24

Met Ala Asp Lys Asp Leu Lys Gly Lys Arg Lys Gln Phe Ile Asn Ser

1

5

10

15

Val Gly Met Gly Thr Val Asn Gly Leu Leu Asp Glu Leu Phe Glu Lys
20 25 30

Asn Val Leu Asn Gln Glu Glu Met Glu Arg Val Lys Cys Glu Asn Ala
35 40 45

Thr Val Met Asp Lys Ala Arg Ala Leu Ile Asp Ser Val Leu Arg Lys
50 55 60

Gly Pro Arg Ala Cys Gln Ile Phe Ile Cys His Ile Cys Glu Glu Asp
65 70 75 80

Thr His Leu Ala Glu Thr Leu Gly Leu Ser Ser Ser Pro Gln Ser Gly
85 90 95

Asn Ser Gln Asn Thr Thr Asp Ser Glu Val Ala Phe Pro Pro Leu Pro
100 105 110

Ala Ser Val Asn Asn Met Pro Gly Pro Ala Glu Pro Glu Glu Ser Val
115 120 125

Asp Ala Leu Lys Leu Cys Pro Arg Glu Asn Phe Val Lys Leu Cys Lys
130 135 140

Gln Arg Ala Glu Glu Ile Tyr Pro Ile Lys Glu Arg Lys Asp Arg Thr
145 150 155 160

Arg Leu Ala Leu Ile Ile Cys Asn Thr Thr Phe Asp His Leu Ser Leu
165 170 175

Arg Lys Gly Ala Asp Leu Asp Val Ala Gly Met Arg Arg Leu Leu Thr
180 185 190

Asp Leu Gly Tyr Ser Val His Ile Lys Glu Glu Leu Thr Ala Lys Asp
195 200 205

Met Glu Ser Glu Leu Arg Ala Phe Ala Ala Arg Pro Glu His Lys Ser
210 215 220

Ser Asp Ser Thr Phe Leu Val Phe Met Ser His Gly Ile Leu Ser Gly
225 230 235 240

Ile Cys Gly Thr Lys Tyr Ser Ala Glu Gly Asp Pro Asp Val Leu Ala
245 250 255

Tyr Asp Thr Ile Phe Gln Ile Phe Asn Asn Arg Asn Cys Leu Ser Leu
260 265 270

Lys Asp Lys Pro Lys Val Ile Ile Val Gln Ala Cys Arg Gly Glu Asn
275 280 285

Leu Gly Glu Leu Leu Ile Ser Asp Ser Pro Ala Ala Pro Met Asp Ser
290 295 300

Thr Ser Gln Met Gly Ser Ser Leu Ser Gln Val Gly Asp Asn Leu Glu
305 310 315 320

Asp Asp Ala Ile Tyr Lys Val His Val Glu Lys Asp Phe Ile Ala Phe
325 330 335

Cys Ser Ser Thr Pro His His Val Ser Trp Arg Asp Val Asn Lys Gly
340 345 350

Ser Leu Phe Ile Thr Gln Leu Ile Thr Cys Phe Gln Lys Tyr Ser Trp
355 360 365

Cys Phe His Leu Glu Glu Val Phe Arg Lys Val Gln Gln Ser Phe Glu
370 375 380

Lys Pro Asn Val Arg Ala Gln Met Pro Thr Ile Glu Arg Leu Ser Met
385 390 395 400

Thr Arg Tyr Phe Tyr Leu Phe Pro Gly Asn
405 410

<210> 25
<211> 1230
<212> DNA
<213> Felis catus

<400> 25
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aaagcaccac gaatactttt ggaagcacgt gatgagttgt gtaatgaaga gagatccctt 180

tttcacgtct ctccaagaca catgatgtgg ggtcgaggag cagaaagcga tgaagtccctt 240
ctccacgtgg accttgtaaa tggcgctgct ctctaggttg tcacccacct gtgaaaggct 300
gctaccatc tgtgaagtgc tgtccattgg ggccgctgga gagtcactga tcaacagttc 360
ccccaaattt tcacctctgc aggccctggac gatgatgacc ttgggcttgc ccttagact 420
aaggcagttg cggttgttga aaatctggaa gatggtgtca taagccaata catctgggtc 480
tccttcagcg ctgtacttcg tcccacagat tccactcagg atgccatgag acatgaacac 540
caggaatgtg ctgtccgagg acttgtgctc tggacgggca gcaaatgccc tcagctctga 600
ttccatgtcc ttagcagtga gttcccttt tatgtgcaca ctgtagccaa ggtctgttaag 660
cagcctcctc atccctgcaa cgtcaaggtc agcccccttc ctgagagaaa gatgatcgaa 720
cgctgtattt catatgtga gagccagacg agtacgatcc tttctcttct ttattggta 780
gatctttca gccctctgtt tacacagttt cacgaagttt tcacgaggac aaagcttgag 840
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aggagaaaaac gctacttcag agtccgtggt gttctgagaa tttccagatt gtgggcttga 960
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ctggcacgcc cgtggccctt tccgcaggac gctgtcgatc agagctcggg cttgtccat 1080
aacggtagcg tttcacatt ttactctctc catctcctcc tggttcagca cgttttctc 1140
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cctcttgccc tttagatcct tgtcggccat 1230

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<210> 26  
<211> 921  
<212> DNA  
<213> Felis catus
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<220>
<221> CDS
<222> (1) .. (921)

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<400>  26
ata tgg gaa ctg gag aaa aac gtt tat gtt gta gag ttg gac tgg cac 48
Ile Trp Glu Leu Glu Lys Asn Val Tyr Val Val Glu Leu Asp Trp His
1           5                  10                   15

cct gat gcc ccc gga gaa atg gtg gtc ctc acc tgc aat act cct gaa 96
Pro Asp Ala Pro Gly Glu Met Val Val Leu Thr Cys Asn Thr Pro Glu
          20                 25                   30

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gaa gat gac atc acc tgg acc tct gac cag agc agt gaa gtc cta ggc Glu Asp Asp Ile Thr Trp Thr Ser Asp Gln Ser Ser Glu Val Leu Gly 35 40 45	144
tct ggt aaa act ctg acc atc caa gtc aaa gaa ttt gca gat gct ggc Ser Gly Lys Thr Leu Thr Ile Gln Val Lys Glu Phe Ala Asp Ala Gly 50 55 60	192
cag tat acc tgt cat aaa gga ggc gag gtt ctg agc cat tcg ttc ctc Gln Tyr Thr Cys His Lys Gly Gly Glu Val Leu Ser His Ser Phe Leu 65 70 75 80	240
ctg ata cac aaa aag gaa gat gga att tgg tcc act gat atc tta agg Leu Ile His Lys Lys Glu Asp Gly Ile Trp Ser Thr Asp Ile Leu Arg 85 90 95	288
gaa cag aaa gaa tcc aaa aat aag atc ttt cta aaa tgt gag gca aag Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe Leu Lys Cys Glu Ala Lys 100 105 110	336
aat tat tct gga cgt ttc acc tgc tgg tgg ctg acg gca atc agt acc Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp Leu Thr Ala Ile Ser Thr 115 120 125	384
gat ttg aaa ttc act gtc aaa agc agc aga ggc tcc tct gac ccc caa Asp Leu Lys Phe Thr Val Lys Ser Ser Arg Gly Ser Ser Asp Pro Gln 130 135 140	432
gag gtg act tgt gga gca gcg aca ctc tca gca gag aag gtc aga gtg Glu Val Thr Cys Gly Ala Ala Thr Leu Ser Ala Glu Lys Val Arg Val 145 150 155 160	480
gac aac agg gat tat aag aag tac aca gtg gag tgt cag gag ggc agt Asp Asn Arg Asp Tyr Lys Tyr Thr Val Glu Cys Gln Glu Gly Ser 165 170 175	528
gcc tgc ccg gct gcc gag gag agc cta ccc att gaa gtc gtg gtg gac Ala Cys Pro Ala Ala Glu Ser Leu Pro Ile Glu Val Val Val Asp 180 185 190	576
gct att cac aag ctc aag tac gaa aac tac acc agc agc ttc ttc atc Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr Thr Ser Ser Phe Phe Ile 195 200 205	624
agg gac atc atc aaa ccg gac cca ccc aag aac ctg caa ctg aag cca Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn Leu Gln Leu Lys Pro 210 215 220	672
tta aaa aat tct cgg cat gtg gaa gtg agc tgg gaa tac cct gac acc Leu Lys Asn Ser Arg His Val Glu Val Ser Trp Glu Tyr Pro Asp Thr 225 230 235 240	720
tgg agc acc cca cat tcc tac ttc tcc tta aca ttt ggc gta cag gtc Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr Phe Gly Val Gln Val 245 250 255	768
cag ggc aag aac aac aga gaa aag aaa gac aga ctc tcc gtg gac aag	816

Gln	Gly	Lys	Asn	Asn	Arg	Glu	Lys	Asp	Arg	Leu	Ser	Val	Asp	Lys		
260						265							270			
acc	tca	gcc	aag	gtc	gtg	tgc	cac	aag	gat	gcc	aag	atc	cgc	gtg	caa	864
Thr	Ser	Ala	Lys	Val	Val	Cys	His	Lys	Asp	Ala	Lys	Ile	Arg	Val	Gln	
275						280							285			
gcc	aga	gac	cgc	tac	tat	agc	tca	tcc	tgg	agc	aac	tgg	gca	tcc	gtg	912
Ala	Arg	Asp	Arg	Tyr	Tyr	Ser	Ser	Ser	Trp	Ser	Asn	Trp	Ala	Ser	Val	
290						295							300			
tcc	tgc	agt														921
Ser	Cys	Ser														
305																
<210>	27															
<211>	307															
<212>	PRT															
<213>	Felis catus															
<400>	27															
Ile	Trp	Glu	Leu	Glu	Lys	Asn	Val	Tyr	Val	Val	Glu	Leu	Asp	Trp	His	
1						5					10				15	
Pro	Asp	Ala	Pro	Gly	Glu	Met	Val	Val	Leu	Thr	Cys	Asn	Thr	Pro	Glu	
20											25				30	
Glu	Asp	Asp	Ile	Thr	Trp	Thr	Ser	Asp	Gln	Ser	Ser	Glu	Val	Leu	Gly	
35												40			45	
Ser	Gly	Lys	Thr	Leu	Thr	Ile	Gln	Val	Lys	Glu	Phe	Ala	Asp	Ala	Gly	
50											55				60	
Gln	Tyr	Thr	Cys	His	Lys	Gly	Gly	Glu	Val	Leu	Ser	His	Ser	Phe	Leu	
65										70				75		80
Leu	Ile	His	Lys	Lys	Glu	Asp	Gly	Ile	Trp	Ser	Thr	Asp	Ile	Leu	Arg	
														85		95
Glu	Gln	Lys	Glu	Ser	Lys	Asn	Lys	Ile	Phe	Leu	Lys	Cys	Glu	Ala	Lys	
														100		110
Asn	Tyr	Ser	Gly	Arg	Phe	Thr	Cys	Trp	Trp	Leu	Thr	Ala	Ile	Ser	Thr	
115														120		125
Asp	Leu	Lys	Phe	Thr	Val	Lys	Ser	Ser	Arg	Gly	Ser	Ser	Asp	Pro	Gln	
130											135				140	

Glu Val Thr Cys Gly Ala Ala Thr Leu Ser Ala Glu Lys Val Arg Val
145 150 155 160

Asp Asn Arg Asp Tyr Lys Tyr Thr Val Glu Cys Gln Glu Gly Ser
165 170 175

Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro Ile Glu Val Val Val Asp
180 185 190

Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr Thr Ser Ser Phe Phe Ile
195 200 205

Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn Leu Gln Leu Lys Pro
210 215 220

Leu Lys Asn Ser Arg His Val Glu Val Ser Trp Glu Tyr Pro Asp Thr
225 230 235 240

Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr Phe Gly Val Gln Val
245 250 255

Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp Arg Leu Ser Val Asp Lys
260 265 270

Thr Ser Ala Lys Val Val Cys His Lys Asp Ala Lys Ile Arg Val Gln
275 280 285

Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp Ser Asn Trp Ala Ser Val
290 295 300

Ser Cys Ser
305

<210> 28
<211> 921
<212> DNA
<213> Felis catus

<400> 28
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cacgcggatc ttggcatcct tgtggcacac gacctggct gaggtcttgt ccacggagag 120
tctgtcttgc ttttctctgt ttttcttgcc ctggacctgt acgccaaatg ttaaggagaa 180

gtaggaatgt	ggggtgctcc	aggtgtcagg	gtattccag	ctcaattcca	catgccaga	240
atttttaat	ggcttcagtt	gcaggttctt	gggtgggtcc	ggttgatga	tgtccctgat	300
gaagaagctg	ctggtgttagt	tttcgtactt	gagcttgtga	atagcgtcca	ccacgacttc	360
aatgggttagg	cttcctcg	cagccggca	ggcactgccc	tcctgacact	ccactgtgta	420
cttcttataa	tccctgttgt	ccactctgac	cttctctgct	gagagtgtcg	ctgctccaca	480
agtacacctct	tgggggtcag	aggagcctct	gctgctttg	acagtgaatt	tcaaatcggt	540
actgattgcc	gtcagccacc	agcaggtgaa	acgtccagaa	taattcttg	cctcacattt	600
tagaaagatc	ttattttgg	attcttctg	ttcccttaag	atatcagtgg	accaaattcc	660
atcttcctt	ttgtgtatca	ggaggaacga	atggctcaga	acctcgccctc	ctttatgaca	720
ggtatactgg	ccagcatctg	caaattctt	gacttggatg	gtcagagttt	taccagagcc	780
taggacttca	ctgctctggt	cagaggtcca	ggtgatgtca	tcttcttcag	gagtattgca	840
ggtgaggacc	accatttctc	cggggccatc	agggtgccag	tccaactcta	caacataaac	900
gttttctcc	agttccata	t				921

<210> 29
 <211> 987
 <212> DNA
 <213> Felis catus

<220>
 <221> CDS
 <222> (1)..(987)

<400> 29	
atg cat cct cag cag ttg gtc atc gcc tgg ttt tcc ctg gtt ttg ctg	48
Met His Pro Gln Gln Leu Val Ile Ala Trp Phe Ser Leu Val Leu Leu	
1 5 10 15	
gca cct ccc ctc atg gcc ata tgg gaa ctg gag aaa aac gtt tat gtt	96
Ala Pro Pro Leu Met Ala Ile Trp Glu Leu Glu Lys Asn Val Tyr Val	
20 25 30	
gta gag ttg gac tgg cac cct gat gcc ccc gga gaa atg gtg gtc ctc	144
Val Glu Leu Asp Trp His Pro Asp Ala Pro Gly Glu Met Val Val Leu	
35 40 45	
acc tgc aat act cct gaa gaa gat gac atc acc tgg acc tct gac cag	192
Thr Cys Asn Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser Asp Gln	
50 55 60	
agc agt gaa gtc cta ggc tct ggt aaa act ctg acc atc caa gtc aāa	240
Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys	

65	70	75	80													
gaa ttt gca gat gct ggc cag tat acc tgt cat aaa gga ggc gag gtt				288												
Glu	Phe	Ala	Asp	Ala	Gly	Gln	Tyr	Thr	Cys	His	Lys	Gly	Gly	Glu	Val	
85															95	
ctg agc cat tcg ttc ctc ctg ata cac aaa aag gaa gat gga att tgg				336												
Leu	Ser	His	Ser	Phe	Leu	Leu	Ile	His	Lys	Lys	Glu	Asp	Gly	Ile	Trp	
100															110	
tcc act gat atc tta agg gaa cag aaa gaa tcc aaa aat aag atc ttt				384												
Ser	Thr	Asp	Ile	Leu	Arg	Glu	Gln	Lys	Glu	Ser	Lys	Asn	Lys	Ile	Phe	
115															125	
cta aaa tgt gag gca aag aat tat tct gga cgt ttc acc tgc tgg tgg				432												
Leu	Lys	Cys	Glu	Ala	Lys	Asn	Tyr	Ser	Gly	Arg	Phe	Thr	Cys	Trp	Trp	
130															140	
ctg acg gca atc agt acc gat ttg aaa ttc act gtc aaa agc agc aga				480												
Leu	Thr	Ala	Ile	Ser	Thr	Asp	Leu	Lys	Phe	Thr	Val	Lys	Ser	Ser	Arg	
145															155	
ggc tcc tct gac ccc caa ggg gtg act tgt gga gca gcg aca ctc tca				528												
Gly	Ser	Ser	Asp	Pro	Gln	Gly	Val	Thr	Cys	Gly	Ala	Ala	Thr	Leu	Ser	
165															175	
gca gag aag gtc aga gtg gac aac agg gat tat aag aag tac aca gtg				576												
Ala	Glu	Lys	Val	Arg	Val	Asp	Asn	Arg	Asp	Tyr	Lys	Tys	Tyr	Thr	Val	
180															190	
gag tgt cag gag ggc agt gcc tgc ccg gct gcc gag gag agc cta ccc				624												
Glu	Cys	Gln	Glu	Gly	Ser	Ala	Cys	Pro	Ala	Ala	Glu	Glu	Ser	Leu	Pro	
195															205	
att gaa gtc gtg gtg gac gct att cac aag ctc aag tac gaa aac tac				672												
Ile	Glu	Val	Val	Asp	Ala	Ile	His	Lys	Leu	Lys	Tyr	Glu	Asn	Tyr		
210															220	
acc agc agc ttc ttc atc agg gac atc atc aaa ccg gac cca ccc aag				720												
Thr	Ser	Ser	Phe	Phe	Ile	Arg	Asp	Ile	Ile	Lys	Pro	Asp	Pro	Pro	Lys	
225															240	
aac ctg caa ctg aag cca tta aaa aat tct cgg cat gtg gaa gtg agc				768												
Asn	Leu	Gln	Leu	Lys	Pro	Leu	Lys	Asn	Ser	Arg	His	Val	Glu	Val	Ser	
245															255	
tgg gaa tac cct gac acc tgg agc acc cca cat tcc tac ttc tcc tta				816												
Trp	Glu	Tyr	Pro	Asp	Thr	Trp	Ser	Thr	Pro	His	Ser	Tyr	Phe	Ser	Leu	
260															270	
aca ttt ggc gta cag gtc cag ggc aag aac aac aga gaa aag aaa gac				864												
Thr	Phe	Gly	Val	Gln	Val	Gln	Gly	Lys	Asn	Asn	Arg	Glu	Lys	Lys	Asp	
275															285	
aga ctc tcc gtg gac aag acc tca gcc aag gtc gtg tgc cac aag gat				912												
Arg	Leu	Ser	Val	Asp	Lys	Thr	Ser	Ala	Lys	Val	Val	Cys	His	Lys	Asp	
290															300	

gcc aag atc cgc gtg caa gcc aga gac cgc tac tat agc tca tcc tgg	960
Ala Lys Ile Arg Val Gln Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp	
305	310
315	320
agc aac tgg gca tcc gtg tcc tgc agt	987
Ser Asn Trp Ala Ser Val Ser Cys Ser	
325	
<210> 30	
<211> 329	
<212> PRT	
<213> Felis catus	
<400> 30	
Met His Pro Gln Gln Leu Val Ile Ala Trp Phe Ser Leu Val Leu Leu	
1	5
10	15
Ala Pro Pro Leu Met Ala Ile Trp Glu Leu Glu Lys Asn Val Tyr Val	
20	25
30	
Val Glu Leu Asp Trp His Pro Asp Ala Pro Gly Glu Met Val Val Leu	
35	40
45	
Thr Cys Asn Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser Asp Gln	
50	55
60	
Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys	
65	70
75	80
Glu Phe Ala Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu Val	
85	90
95	
Leu Ser His Ser Phe Leu Leu Ile His Lys Lys Glu Asp Gly Ile Trp	
100	105
110	
Ser Thr Asp Ile Leu Arg Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe	
115	120
125	
Leu Lys Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp	
130	135
140	
Leu Thr Ala Ile Ser Thr Asp Leu Lys Phe Thr Val Lys Ser Ser Arg	
145	150
155	160

Gly Ser Ser Asp Pro Gln Gly Val Thr Cys Gly Ala Ala Thr Leu Ser
165 170 175

Ala Glu Lys Val Arg Val Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val
180 185 190

Glu Cys Gln Glu Gly Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro
195 200 205

Ile Glu Val Val Val Asp Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr
210 215 220

Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys
225 230 235 240

Asn Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg His Val Glu Val Ser
245 250 255

Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu
260 265 270

Thr Phe Gly Val Gln Val Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp
275 280 285

Arg Leu Ser Val Asp Lys Thr Ser Ala Lys Val Val Cys His Lys Asp
290 295 300

Ala Lys Ile Arg Val Gln Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp
305 310 315 320

Ser Asn Trp Ala Ser Val Ser Cys Ser
325

<210> 31
<211> 987
<212> DNA
<213> Felis catus

<400> 31
actgcaggac acggatgccc agttgctcca ggatgagcta tagtagcggt ctctggcttg 60
cacgcggatc ttggcatcct tgtggcacac gacctggct gaggtcttgtt ccacggagag 120
tctgtcttcc ttttctctgt ttttcttgcc ctggacctgt acgccaaatg ttaaggagaa 180
gttaggaatgt ggggtgctcc aggtgtcagg gtattccag ctcacttcca catgccgaga 240

attttttaat ggcttcagtt gcaggttctt ggggtgggtcc ggtttgatga tgcctcgat	300
gaagaagctg ctggtgttagt ttctgtactt gagcttgcata atagcgtcca ccacgacttc	360
aatgggtagg ctctcctcgg cagccggca ggcactgccc tcctgacact ccactgtgta	420
cttcttataa tccctgttgtt ccactctgac cttctgtgtt gagagtgtcg ctgctccaca	480
agtcacccct tgggggtcag aggagcctct gctgctttt acagtgaatt tcaaatcggt	540
actgattgcc gtcagccacc agcaggtgaa acgtccagaa taattcttt cctcacattt	600
tagaaagatc ttatTTTgg attcttctg ttcccttaag atatcagtgg accaaattcc	660
atcttccttt ttgtgtatca ggaggaacga atggctcaga acctcgccctc ctatgtaca	720
ggtatactgg ccagcatctg caaattctt gacttggatg gtcagatgtt taccagagcc	780
taggacttca ctgctctggt cagaggtcca ggtgatgtca tcttcttcag ggttattgca	840
ggtgaggacc accatttctc cgggggcattc agggtgccag tccaaactcta caacataaac	900
gttttctcc agttccata tgccatgag gggaggtgcc agcaaaacca gggaaaacca	960
ggcgatgacc aactgctgag gatgcat	987

<210> 32
 <211> 666
 <212> DNA
 <213> Felis catus

<220>
 <221> CDS
 <222> (1)..(666)

atg tgc ccg ccg cgt ggc ctc ctc ctt gta acc atc ctg gtc ctg tta	48
Met Cys Pro Pro Arg Gly Leu Leu Leu Val Thr Ile Leu Val Leu Leu	
1 5 10 15	
aac cac ctg gac cac ctc agt ttg gcc agg aac ctc ccc aca ccc aca	96
Asn His Leu Asp His Leu Ser Leu Ala Arg Asn Leu Pro Thr Pro Thr	
20 25 30	
cca agc cca gga atg ttc cag tgc ctc aac cac tcc caa acc ctg ctg	144
Pro Ser Pro Gly Met Phe Gln Cys Leu Asn His Ser Gln Thr Leu Leu	
35 40 45	
cga gcc atc agc aac acg ctt cag aag gcc aga caa act cta gaa ttt	192
Arg Ala Ile Ser Asn Thr Leu Gln Lys Ala Arg Gln Thr Leu Glu Phe	
50 55 60	
tac tcc tgc act tcc gaa gag att gat cat gaa gat atc aca aaa gat	240
Tyr Ser Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp	

65	70	75	80	
aaa acc agc aca gtg gag gcc tgc tta cca ctg gaa tta acc atg aat Lys Thr Ser Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Met Asn 85 90 95				288
gag agt tgc ctg gct tcc aga gag atc tct ctg ata act aat ggg agt Glu Ser Cys Leu Ala Ser Arg Glu Ile Ser Leu Ile Thr Asn Gly Ser 100 105 110				336
tgc ctg gcc tcc aga aag acc tct ttt atg acg acc ctg tgc ctt agc Cys Leu Ala Ser Arg Lys Thr Ser Phe Met Thr Thr Leu Cys Leu Ser 115 120 125				384
agt atc tat gag gac ttg aag atg tac cag gtg gag ttc aag gcc atg Ser Ile Tyr Glu Asp Leu Lys Met Tyr Gln Val Glu Phe Lys Ala Met 130 135 140				432
aat gca aag ctg tta atg gat cct aaa agg cag atc ttt ctg gat caa Asn Ala Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln 145 150 155 160				480
aac atg ctg aca gct att gat gag ctg tta cag gcc ctg aat gtc aac Asn Met Leu Thr Ala Ile Asp Glu Leu Leu Gln Ala Leu Asn Val Asn 165 170 175				528
agt gtg act gtg cca cag aac tcc tcc ctg gaa gaa ccg gat ttt tat Ser Val Thr Val Pro Gln Asn Ser Ser Leu Glu Glu Pro Asp Phe Tyr 180 185 190				576
aaa act aaa atc aag ctc tgc ata ctt ctt cat gct ttc aga att cgt Lys Thr Lys Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg 195 200 205				624
gca gtg acc atc aat aga atg atg agc tat ctg aat gct tcc Ala Val Thr Ile Asn Arg Met Met Ser Tyr Leu Asn Ala Ser 210 215 220				666
<210> 33				
<211> 222				
<212> PRT				
<213> Felis catus				
<400> 33				
Met Cys Pro Pro Arg Gly Leu Leu Leu Val Thr Ile Leu Val Leu Leu 1 5 10 15				
Asn His Leu Asp His Leu Ser Leu Ala Arg Asn Leu Pro Thr Pro Thr 20 25 30				
Pro Ser Pro Gly Met Phe Gln Cys Leu Asn His Ser Gln Thr Leu Leu 35 40 45				

Arg Ala Ile Ser Asn Thr Leu Gln Lys Ala Arg Gln Thr Leu Glu Phe
50 55 60

Tyr Ser Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp
65 70 75 80

Lys Thr Ser Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Met Asn
85 90 95

Glu Ser Cys Leu Ala Ser Arg Glu Ile Ser Leu Ile Thr Asn Gly Ser
100 105 110

Cys Leu Ala Ser Arg Lys Thr Ser Phe Met Thr Thr Leu Cys Leu Ser
115 120 125

Ser Ile Tyr Glu Asp Leu Lys Met Tyr Gln Val Glu Phe Lys Ala Met
130 135 140

Asn Ala Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln
145 150 155 160

Asn Met Leu Thr Ala Ile Asp Glu Leu Leu Gln Ala Leu Asn Val Asn
165 170 175

Ser Val Thr Val Pro Gln Asn Ser Ser Leu Glu Glu Pro Asp Phe Tyr
180 185 190

Lys Thr Lys Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg
195 200 205

Ala Val Thr Ile Asn Arg Met Met Ser Tyr Leu Asn Ala Ser
210 215 220

<210> 34
<211> 666
<212> DNA
<213> Felis catus

<400> 34
ggaaggattc agatagctca tcattctatt gatggtaact gcacgaattc tgaaagcatg 60
aagaagtatg cagagcttga ttttagttt ataaaaatcc ggttcttcca gggaggagtt 120
ctgtggcaca gtcacactgt tgacattcag ggcctgtaac agctcatcaa tagctgtcag 180

catgtttga tccagaaaaga tctgcctttt aggatccatt aacagcttg cattcatggc	240
cttgaactcc acctggtaca tcttcaagtc ctcatagata ctgctaaggc acagggtcgt	300
cataaaaagag gtctttctgg aggccaggca actcccatta gttatcagag agatctct	360
ggaagccagg caactctcat tcatggtaa ttccagtgg aagcaggcct ccactgtgct	420
ggtttatct tttgtgatat ctcatgatc aatctttcg gaagtgcagg agtaaaattc	480
tagagttgt ctggccttct gaagcgtgtt gctgatggct cgacgcaggg tttggagtg	540
gttggggcac tggaacattc ctgggcttgg tgtgggtgtg gggaggttcc tggccaaact	600
gaggtggtcc aggtggttta acaggaccag gatggttaca aggaggaggc cacgcggcgg	660
gcacat	666

<210> 35
 <211> 591
 <212> DNA
 <213> Felis catus

<220>
 <221> CDS
 <222> (1)..(591)

<400> 35	
agg aac ctc ccc aca ccc aca cca agc cca gga atg ttc cag tgc ctc	48
Arg Asn Leu Pro Thr Pro Ser Pro Gly Met Phe Gln Cys Leu	
1 5 10 15	
aac cac tcc caa acc ctg ctg cga gcc atc agc aac acg ctt cag aag	96
Asn His Ser Gln Thr Leu Leu Arg Ala Ile Ser Asn Thr Leu Gln Lys	
20 25 30	
gcc aga caa act cta gaa ttt tac tcc tgc act tcc gaa gag att gat	144
Ala Arg Gln Thr Leu Glu Phe Tyr Ser Cys Thr Ser Glu Glu Ile Asp	
35 40 45	
cat gaa gat atc aca aaa gat aaa acc agc aca gtg gag gcc tgc tta	192
His Glu Asp Ile Thr Lys Asp Lys Thr Ser Thr Val Glu Ala Cys Leu	
50 55 60	
cca ctg gaa tta acc atg aat gag agt tgc ctg gct tcc aga gag atc	240
Pro Leu Glu Leu Thr Met Asn Glu Ser Cys Leu Ala Ser Arg Glu Ile	
65 70 75 80	
tct ctg ata act aat ggg agt tgc ctg gcc tcc aga aag acc tct ttt	288
Ser Leu Ile Thr Asn Gly Ser Cys Leu Ala Ser Arg Lys Thr Ser Phe	
85 90 95	
atg acg acc ctg tgc ctt agc agt atc tat gag gac ttg aag atg tac	336
Met Thr Thr Leu Cys Leu Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr	
100 105 110	

cag gtg gag ttc aag gcc atg aat gca aag ctg tta atg gat cct aaa 384
Gln Val Glu Phe Lys Ala Met Asn Ala Lys Leu Leu Met Asp Pro Lys
115 120 125

agg cag atc ttt ctg gat caa aac atg ctg aca gct att gat gag ctg 432
Arg Gln Ile Phe Leu Asp Gln Asn Met Leu Thr Ala Ile Asp Glu Leu
130 135 140

tta cag gcc ctg aat gtc aac agt gtg act gtg cca cag aac tcc tcc 480
Leu Gln Ala Leu Asn Val Asn Ser Val Thr Val Pro Gln Asn Ser Ser
145 150 155 160

ttg gaa gaa ccg gat ttt tat aaa act aaa atc aag ctc tgc ata ctt 528
Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu
165 170 175

ctt cat gct ttc aga att cgt gca gtg acc atc aat aga atg atg agc 576
Leu His Ala Phe Arg Ile Arg Ala Val Thr Ile Asn Arg Met Met Ser
180 185 190

tat ctg aat gct tcc 591
Tyr Leu Asn Ala Ser
195

<210> 36
<211> 197
<212> PRT
<213> Felis catus

<400> 36

Arg Asn Leu Pro Thr Pro Thr Pro Ser Pro Gly Met Phe Gln Cys Leu 1
1 5 10 15

Asn His Ser Gln Thr Leu Leu Arg Ala Ile Ser Asn Thr Leu Gln Lys
20 25 30

Ala Arg Gln Thr Leu Glu Phe Tyr Ser Cys Thr Ser Glu Glu Ile Asp
35 40 45

His Glu Asp Ile Thr Lys Asp Lys Thr Ser Thr Val Glu Ala Cys Leu
50 55 60

Pro Leu Glu Leu Thr Met Asn Glu Ser Cys Leu Ala Ser Arg Glu Ile
65 70 75 80

Ser Leu Ile Thr Asn Gly Ser Cys Leu Ala Ser Arg Lys Thr Ser Phe
85 90 95

Met Thr Thr Leu Cys Leu Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr
100 105 110

Gln Val Glu Phe Lys Ala Met Asn Ala Lys Leu Leu Met Asp Pro Lys
115 120 125

Arg Gln Ile Phe Leu Asp Gln Asn Met Leu Thr Ala Ile Asp Glu Leu
130 135 140

Leu Gln Ala Leu Asn Val Asn Ser Val Thr Val Pro Gln Asn Ser Ser
145 150 155 160

Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu
165 170 175

Leu His Ala Phe Arg Ile Arg Ala Val Thr Ile Asn Arg Met Met Ser
180 185 190

Tyr Leu Asn Ala Ser
195

<210> 37
<211> 591
<212> DNA
<213> Felis catus

<400> 37
ggaagcattc agatacgctca tcattctatt gatggtcact gcacgaattc tgaaagcatg 60
aagaagtatg cagagcttga ttttagttt ataaaaatcc gggttcttcca aggaggagtt 120
ctgtggcaca gtcacactgt tgacattcag ggcctgtaac agctcatcaa tagctgtcag 180
catgtttga tccagaaaaga tctgcctttt aggatccatt aacagcttg cattcatggc 240
cttgaactcc acctggtaca tcttcaagtc ctcatagata ctgctaaggc acagggtcgt 300
cataaaagag gtctttctgg aggccaggca actcccatta gttatcagag agatctct 360
ggaagccagg caactctcat tcatggtaa ttccagtggt aagcaggcct ccactgtgct 420
ggttttatct tttgtgatat ctcatgatc aatctttcg gaagtgcagg agtaaaattc 480
tagagtttgt ctggccttct gaagcgtgtt gctgatggct cgacgcagg tttgggagtg 540
gttgaggcac tggAACATTc ctgggcttgg tgtgggtgtg gggaggttcc t 591

<210> 38
<211> 1599

<212> DNA
<213> Felis catus

<220>
<221> CDS
<222> (1)..(1599)

<400> 38

atg cat cct cag cag ttg gtc atc gcc tgg ctt tcc ctg gtt ttg ctg	48
Met His Pro Gln Gln Leu Val Ile Ala Trp Leu Ser Leu Val Leu Leu	
1 5 10 15	
gca cct ccc ctc atg gcc ata tgg gaa ctg gag aaa aac gtt tat gtt	96
Ala Pro Pro Leu Met Ala Ile Trp Glu Leu Glu Lys Asn Val Tyr Val	
20 25 30	
gta gag ttg gac tgg cac cct gat gcc ccc gga gaa atg gtg gtc ctc	144
Val Glu Leu Asp Trp His Pro Asp Ala Pro Gly Glu Met Val Val Leu	
35 40 45	
acc tgc aat act cct gaa gaa gat gac atc acc tgg acc tct gac cag	192
Thr Cys Asn Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser Asp Gln	
50 55 60	
agc agt gaa gtc cta ggc tct ggt aaa act ctg acc atc caa gtc aaa	240
Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys	
65 70 75 80	
gaa ttt gca gat gct ggc cag tat acc tgt cat aaa gga ggc gag gtt	288
Glu Phe Ala Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu Val	
85 90 95	
ctg agc cat tcg ttc ctc ctg ata cac aaa aag gaa gat gga att tgg	336
Leu Ser His Ser Phe Leu Leu Ile His Lys Lys Glu Asp Gly Ile Trp	
100 105 110	
tcc act gat atc tta agg gaa cag aaa gaa tcc aaa aat aag atc ttt	384
Ser Thr Asp Ile Leu Arg Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe	
115 120 125	
cta aaa tgt gag gca aag aat tat tct gga cgt ttc acc tgc tgg tgg	432
Leu Lys Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp	
130 135 140	
ctg acg gca atc agt acc gat ttg aaa ttc act gtc aaa agc agc aga	480
Leu Thr Ala Ile Ser Thr Asp Leu Lys Phe Thr Val Lys Ser Ser Arg	
145 150 155 160	
ggc tcc tct gac ccc caa gag gtg act tgt gga gca gcg aca ctc tca	528
Gly Ser Ser Asp Pro Gln Glu Val Thr Cys Gly Ala Ala Thr Leu Ser	
165 170 175	
gca gag aag gtc aga gtg gac aac agg gat tat aag aag tac aca gtg	576
Ala Glu Lys Val Arg Val Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val	
180 185 190	

gag tgc cag gag ggc agt gcc tgc ccg gct gcc gag gag agc cta ccc Glu Cys Gln Glu Gly Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro 195 200 205	624
att gaa gtc gtg gtc gac gct att cac aag ctc aag tac gaa aac tac Ile Glu Val Val Val Asp Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr 210 215 220	672
acc agc agc ttc ttc atc agg gac atc atc aaa ccg gac cca ccc aag Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys 225 230 235 240	720
aac ctg caa ctg aag cca tta aaa aat tct cgg cat gtg gaa gtg agc Asn Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg His Val Glu Val Ser 245 250 255	768
tgg gaa tac cct gac acc tgg agc acc cca cat tcc tac ttc tcc tta Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu 260 265 270	816
aca ttt ggc gta cag gtc cag ggc aag aac aac aga gaa aag aaa gac Thr Phe Gly Val Gln Val Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp 275 280 285	864
aga ctc tcc gtg gac aag acc tca gcc aag gtc gtg tgc cac aag gat Arg Leu Ser Val Asp Lys Thr Ser Ala Lys Val Val Cys His Lys Asp 290 295 300	912
gcc aag atc cgc gtg caa gcc aga gac cgc tac tat agc tca tcc tgg Ala Lys Ile Arg Val Gln Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp 305 310 315 320	960
agc aac tgg gca tcc gtg tcc tgc agt ggt ggc ggt ggc ggc gga tct Ser Asn Trp Ala Ser Val Ser Cys Ser Gly Gly Gly Gly Gly Ser 325 330 335	1008
aga aac ttg cca acc cct act cca tcc ccg ggg atg ttc cag tgc ctc Arg Asn Leu Pro Thr Pro Ser Pro Gly Met Phe Gln Cys Leu 340 345 350	1056
aac cac tcc caa acc ctg ctg cga gcc atc agc aac acg ctt cag aag Asn His Ser Gln Thr Leu Leu Arg Ala Ile Ser Asn Thr Leu Gln Lys 355 360 365	1104
gcc aga caa act cta gaa ttt tac tcc tgc act tcc gaa gag att gat Ala Arg Gln Thr Leu Glu Phe Tyr Ser Cys Thr Ser Glu Glu Ile Asp 370 375 380	1152
cat gaa gat atc aca aaa gat aaa acc agc aca gtg gag gcc tgc tta His Glu Asp Ile Thr Lys Asp Lys Thr Ser Thr Val Glu Ala Cys Leu 385 390 395 400	1200
cca ctg gaa tta acc atg aat gag agt tgc ctg gct tcc aga gag atc Pro Leu Glu Leu Thr Met Asn Glu Ser Cys Leu Ala Ser Arg Glu Ile 405 410 415	1248
tct ctg ata act aat ggg agt tgc ctg gcc tcc aga aag acc tct ttt	1296

<210> 39
<211> 533
<212> PRT
<213> *Felis catus*

<400> 39

Met His Pro Gln Gln Leu Val Ile Ala Trp Leu Ser Leu Val Leu Leu
 1 5 10 15

Ala Pro Pro Leu Met Ala Ile Trp Glu Leu Glu Lys Asn Val Tyr Val
20 25 30

Val Glu Leu Asp Trp His Pro Asp Ala Pro Gly Glu Met Val Val Leu
35 ` 40 45

Thr Cys Asn Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser Asp Gln
50 55 60

Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys
65 70 75 80

Glu Phe Ala Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu Val
85 90 95

Leu Ser His Ser Phe Leu Leu Ile His Lys Lys Glu Asp Gly Ile Trp
100 105 110

Ser Thr Asp Ile Leu Arg Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe
115 120 125

Leu Lys Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp
130 135 140

Leu Thr Ala Ile Ser Thr Asp Leu Lys Phe Thr Val Lys Ser Ser Arg
145 150 155 160

Gly Ser Ser Asp Pro Gln Glu Val Thr Cys Gly Ala Ala Thr Leu Ser
165 170 175

Ala Glu Lys Val Arg Val Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val
180 185 190

Glu Cys Gln Glu Gly Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro
195 200 205

Ile Glu Val Val Val Asp Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr
210 215 220

Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys
225 230 235 240

Asn Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg His Val Glu Val Ser
245 250 255

Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu
260 265 270

Thr Phe Gly Val Gln Val Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp
275 280 285

Arg Leu Ser Val Asp Lys Thr Ser Ala Lys Val Val Cys His Lys Asp
290 295 300

Ala Lys Ile Arg Val Gln Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp
305 310 315 320

Ser Asn Trp Ala Ser Val Ser Cys Ser Gly Gly Gly Gly Gly Ser
325 330 335

Arg Asn Leu Pro Thr Pro Thr Pro Ser Pro Gly Met Phe Gln Cys Leu
340 345 350

Asn His Ser Gln Thr Leu Leu Arg Ala Ile Ser Asn Thr Leu Gln Lys
355 360 365

Ala Arg Gln Thr Leu Glu Phe Tyr Ser Cys Thr Ser Glu Glu Ile Asp
370 375 380

His Glu Asp Ile Thr Lys Asp Lys Thr Ser Thr Val Glu Ala Cys Leu
385 390 395 400

Pro Leu Glu Leu Thr Met Asn Glu Ser Cys Leu Ala Ser Arg Glu Ile
405 410 415

Ser Leu Ile Thr Asn Gly Ser Cys Leu Ala Ser Arg Lys Thr Ser Phe
420 425 430

Met Thr Thr Leu Cys Leu Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr
435 440 445

Gln Val Glu Phe Lys Ala Met Asn Ala Lys Leu Leu Met Asp Pro Lys
450 455 460

Arg Gln Ile Phe Leu Asp Gln Asn Met Leu Thr Ala Ile Asp Glu Leu
465 470 475 480

Leu Gln Ala Leu Asn Val Asn Ser Val Thr Val Pro Gln Asn Ser Ser
485 490 495

Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu
500 505 510

Leu His Ala Phe Arg Ile Arg Ala Val Thr Ile Asn Arg Met Met Ser
515 520 525

Tyr Leu Asn Ala Ser
530

<210> 40
<211> 1599
<212> DNA
<213> Felis catus

<400> 40
ggaagcattc agatagctca tcattctatt gatggtaact gcacgaattc taaaaggcatg 60
aagaagtatg cagagcttga ttttagttt ataaaaatcc gggtttcca aggaggagtt 120
ctgtggcaca gtcacactgt tgacattcag ggcctgtaac agctcatcaa tagctgtcag 180
catgtttga tccagaaaga tctgcctttt aggttccatt aacagcttg cattcatggc 240
cttgaactcc acctggtaca tcttcaagtc ctcatagata ctgctaaggc acagggtcgt 300
cataaaagag gtctttctgg aggccaggca actcccatta gttatcagag agatctct 360
ggaagccagg caactctcat tcatggtaa ttccagtggt aaggcaggct ccactgtgct 420
ggtttatct tttgtgatat ctcatgatc aatctttcg gaagtgcagg agtaaaattc 480
tagagtttgt ctggccttct gaagcgtgtt gctgatggct cgccaggcagg tttgggagtg 540
gttggggcac tggaacatcc ccggggatgg agtaggggtt ggcaagtttc tagatccgcc 600
gccaccgcca ccactgcagg acacggatgc ccagttgctc caggatgagc tatagtagcg 660
gtctctggct tgcacgcgga tcttggcattt cttgtggcac acgaccttgg ctgaggtctt 720
gtccacggag agtctgtctt tctttctct gttgttcttgc ccctggacct gtacgccaaa 780
tgttaaggag aagtaggaat gtggggtgct ccaggtgtca gggattccc agctcacttc 840
cacatgccga gaattttta atggcttcag ttgcaggttc ttgggtgggt ccggtttgc 900
gatgtccctg atgaagaagc tgctggtgta gtttcgtac ttgagcttgt gaatagcg 960
caccacgact tcaatggta ggctctcctc ggcagccggg caggcactgc cctcctgaca 1020
ctccactgtg tacttcttat aatccctgtt gtccactctg accttctctg ctgagagtgt 1080
cgctgctcca caagtacact ctgggggtc agaggagct ctgctgttt tgacagtga 1140
tttcaaatacg gtactgattt ccgtcagccca ccagcagggtg aaacgtccag aataattctt 1200
tgccctcacat ttttagaaaga tcttattttt ggatttttc tgccctta agatatcgt 1260
ggacccaaatt ccatcttcct tttgtgtat caggaggaac gaatggctca gaaccccgcc 1320
tcctttatga caggtatact ggccagcatc tgcaaattct ttgacttggaa tggtcagagt 1380
tttaccagag cctaggactt cactgctctg gtcagaggc caggtgatgt catttcttc 1440

aggagtattg caggtgagga ccaccatttc tccggggca tcagggtgcc agtccaactc	1500
tacaacataa acgttttct ccagttccc tatggccatg aggggaggtg ccagcaaaac	1560
cagggaaagc caggcgatga ccaactgctg aggatgcat	1599

<210> 41
<211> 576
<212> DNA
<213> *Felis catus*

<400> 41	
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aaatgagttt gaaaagatct ttctctttt cacaagctag aaagtacccc ttgtacaatg	120
aagactcaaa ttgtatctta tcatcatgtc ctggaacact tctctgaaag aatatgatgt	180
catttccttc atcattgata ctctcaggag gactcatttc cttaaaggaa ataattttgt	240
tctcacagga gagagtagac atggctttat aattcacaga gatggttact gccagacctc	300
tagtgaggct atcttatac atatatatga taaattcagt ccggggtgca ttatctgtac	360
agtcagaatc aggcataatcc tcaaacacag gttgatctcc ctggtaatg aagagaactt	420
ggtcgttcaa gtttcgtaag attgagagtt tatgttcaag cttgccaaag taatctgttt	480
ccaggttttc atcactgtca gctacaaagt aaagtgtatt gtcaataaaat ttcattccca	540
caaagttgat gcaatcatct actggtagat cagtca	576

<210> 42
<211> 0
<212> DNA
<213> *Felis catus*

<400> 42
000

<210> 43
<211> 1533
<212> DNA
<213> *Felis catus*

<220>
<221> CDS
<222> (1)..(1533)

<400> 43			
ata tgg gaa ctg gag aaa aac gtt.tat gtt gta gag ttg gac tgg cac	48		
Ile Trp Glu Leu Glu Lys Asn Val Tyr Val Val Glu Leu Asp Trp His			
1	5	10	15

cct gat gcc ccc gga gaa atg gtg gtc ctc acc tgc aat act cct gaa			96
Pro Asp Ala Pro Gly Glu Met Val Val Leu Thr Cys Asn Thr Pro Glu			
20	25	30	
gaa gat gac atc acc tgg acc tct gac cag agt gaa gtc cta ggc			144
Glu Asp Asp Ile Thr Trp Thr Ser Asp Gln Ser Ser Glu Val Leu Gly			
35	40	45	
tct ggt aaa act ctg acc atc caa gtc aaa gaa ttt gca gat gct ggc			192
Ser Gly Lys Thr Leu Thr Ile Gln Val Lys Glu Phe Ala Asp Ala Gly			
50	55	60	
cag tat acc tgt cat aaa gga ggc gag gtt ctg agc cat tcg ttc ctc			240
Gln Tyr Thr Cys His Lys Gly Gly Glu Val Leu Ser His Ser Phe Leu			
65	70	75	80
ctg ata cac aaa aag gaa gat gga att tgg tcc act gat atc tta agg			288
Leu Ile His Lys Lys Glu Asp Gly Ile Trp Ser Thr Asp Ile Leu Arg			
85	90	95	
gaa cag aaa gaa tcc aaa aat aag atc ttt cta aaa tgt gag gca aag			336
Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe Leu Lys Cys Glu Ala Lys			
100	105	110	
aat tat tct gga cgt ttc acc tgc tgg ctg acg gca atc agt acc			384
Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp Leu Thr Ala Ile Ser Thr			
115	120	125	
gat ttg aaa ttc act gtc aaa agc agc aga ggc tcc tct gac ccc caa			432
Asp Leu Lys Phe Thr Val Lys Ser Ser Arg Gly Ser Ser Asp Pro Gln			
130	135	140	
gag gtg act tgt gga gca gcg aca ctc tca gca gag aag gtc aga gtg			480
Glu Val Thr Cys Gly Ala Ala Thr Leu Ser Ala Glu Lys Val Arg Val			
145	150	155	160
gac aac agg gat tat aag aag tac aca gtg gag tgt cag gag ggc agt			528
Asp Asn Arg Asp Tyr Lys Tyr Thr Val Glu Cys Gln Glu Gly Ser			
165	170	175	
gcc tgc ccg gct gcc gag gag agc cta ccc att gaa gtc gtg gtg gac			576
Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro Ile Glu Val Val Val Asp			
180	185	190	
gct att cac aag ctc aag tac gaa aac tac acc agc agc ttc ttc atc			624
Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr Thr Ser Ser Phe Phe Ile			
195	200	205	
agg gac atc atc aaa ccg gac cca ccc aag aac ctgcaa ctg aag cca			672
Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn Leu Gln Leu Lys Pro			
210	215	220	
tta aaa aat tct cgg cat gtg gaa gtg agc tgg gaa tac cct gac acc			720
Leu Lys Asn Ser Arg His Val Glu Val Ser Trp Glu Tyr Pro Asp Thr			
225	230	235	240

tgg agc acc cca cat tcc tac ttc tcc tta aca ttt ggc gta cag gtc Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr Phe Gly Val Gln Val 245 250 255	768
cag ggc aag aac aac aga gaa aag aaa gac aga ctc tcc gtg gac aag Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp Arg Leu Ser Val Asp Lys 260 265 270	816
acc tca gcc aag gtc gtg tgc cac aag gat gcc aag atc cgc gtg caa Thr Ser Ala Lys Val Val Cys His Lys Asp Ala Lys Ile Arg Val Gln 275 280 285	864
gcc aga gac cgc tac tat agc tca tcc tgg agc aac tgg gca tcc gtg Ala Arg Asp Arg Tyr Tyr Ser Ser Trp Ser Asn Trp Ala Ser Val 290 295 300	912
tcc tgc agt ggt ggc ggt ggc gga tct aga aac ttg cca acc cct Ser Cys Ser Gly Gly Gly Gly Ser Arg Asn Leu Pro Thr Pro 305 310 315 320	960
act cca tcc ccg ggg atg ttc cag tgc ctc aac cac tcc caa acc ctg Thr Pro Ser Pro Gly Met Phe Gln Cys Leu Asn His Ser Gln Thr Leu 325 330 335	1008
ctg cga gcc atc agc aac acg ctt cag aag gcc aga caa act cta gaa Leu Arg Ala Ile Ser Asn Thr Leu Gln Lys Ala Arg Gln Thr Leu Glu 340 345 350	1056
ttt tac tcc tgc act tcc gaa gag att gat cat gaa gat atc aca aaa Phe Tyr Ser Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys 355 360 365	1104
gat aaa acc agc aca gtg gag gcc tgc tta cca ctg gaa tta acc atg Asp Lys Thr Ser Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Met 370 375 380	1152
aat gag agt tgc ctg gct tcc aga gag atc tct ctg ata act aat ggg Asn Glu Ser Cys Leu Ala Ser Arg Glu Ile Ser Leu Ile Thr Asn Gly 385 390 395 400	1200
agt tgc ctg gcc tcc aga aag acc tct ttt atg acg acc ctg tgc ctt Ser Cys Leu Ala Ser Arg Lys Thr Ser Phe Met Thr Thr Leu Cys Leu 405 410 415	1248
agc agt atc tat gag gac ttg aag atg tac cag gtg gag ttc aag gcc Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr Gln Val Glu Phe Lys Ala 420 425 430	1296
atg aat gca aag ctg tta atg gat cct aaa agg cag atc ttt ctg gat Met Asn Ala Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp 435 440 445	1344
caa aac atg ctg aca gct att gat gag ctg tta cag gcc ctg aat gtc Gln Asn Met Leu Thr Ala Ile Asp Glu Leu Leu Gln Ala Leu Asn Val 450 455 460	1392
aac agt gtg act gtg cca cag aac tcc tcc ttg gaa gaa ccg gat ttt	1440

Asn Ser Val Thr Val Pro Gln Asn Ser Ser Leu Glu Glu Pro Asp Phe				
465	470	475	480	
tat aaa act aaa atc aag ctc tgc ata ctt ctt cat gct ttc aga att				1488
Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile				
485	490	495		
cgt gca gtg acc atc aat aga atg atg agc tat ctg aat gct tcc				1533
Arg Ala Val Thr Ile Asn Arg Met Met Ser Tyr Leu Asn Ala Ser				
500	505	510		
<210> 44				
<211> 511				
<212> PRT				
<213> Felis catus				
<400> 44				
Ile Trp Glu Leu Glu Lys Asn Val Tyr Val Val Glu Leu Asp Trp His				
1	5	10	15	
Pro Asp Ala Pro Gly Glu Met Val Val Leu Thr Cys Asn Thr Pro Glu				
20	25	30		
Glu Asp Asp Ile Thr Trp Thr Ser Asp Gln Ser Ser Glu Val Leu Gly				
35	40	45		
Ser Gly Lys Thr Leu Thr Ile Gln Val Lys Glu Phe Ala Asp Ala Gly				
50	55	60		
Gln Tyr Thr Cys His Lys Gly Gly Glu Val Leu Ser His Ser Phe Leu				
65	70	75	80	
Leu Ile His Lys Lys Glu Asp Gly Ile Trp Ser Thr Asp Ile Leu Arg				
85	90	95		
Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe Leu Lys Cys Glu Ala Lys				
100	105	110		
Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp Leu Thr Ala Ile Ser Thr				
115	120	125		
Asp Leu Lys Phe Thr Val Lys Ser Ser Arg Gly Ser Ser Asp Pro Gln				
130	135	140		
Glu Val Thr Cys Gly Ala Ala Thr Leu Ser Ala Glu Lys Val Arg Val				
145	150	155	160	

Asp Asn Arg Asp Tyr Lys Tyr Thr Val Glu Cys Gln Glu Gly Ser
165 170 175

Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro Ile Glu Val Val Val Asp
180 185 190

Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr Thr Ser Ser Phe Phe Ile
195 200 205

Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn Leu Gln Leu Lys Pro
210 215 220

Leu Lys Asn Ser Arg His Val Glu Val Ser Trp Glu Tyr Pro Asp Thr
225 230 235 240

Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr Phe Gly Val Gln Val
245 250 255

Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp Arg Leu Ser Val Asp Lys
260 265 270

Thr Ser Ala Lys Val Val Cys His Lys Asp Ala Lys Ile Arg Val Gln
275 280 285

Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp Ser Asn Trp Ala Ser Val
290 295 300

Ser Cys Ser Gly Gly Gly Gly Ser Arg Asn Leu Pro Thr Pro
305 310 315 320

Thr Pro Ser Pro Gly Met Phe Gln Cys Leu Asn His Ser Gln Thr Leu
325 330 335

Leu Arg Ala Ile Ser Asn Thr Leu Gln Lys Ala Arg Gln Thr Leu Glu
340 345 350

Phe Tyr Ser Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys
355 360 365

Asp Lys Thr Ser Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Met
370 375 380

Asn Glu Ser Cys Leu Ala Ser Arg Glu Ile Ser Leu Ile Thr Asn Gly
385 390 395 400

Ser Cys Leu Ala Ser Arg Lys Thr Ser Phe Met Thr Thr Leu Cys Leu
405 410 415

Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr Gln Val Glu Phe Lys Ala
420 425 430

Met Asn Ala Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp
435 440 445

Gln Asn Met Leu Thr Ala Ile Asp Glu Leu Leu Gln Ala Leu Asn Val
450 455 460

Asn Ser Val Thr Val Pro Gln Asn Ser Ser Leu Glu Glu Pro Asp Phe
465 470 475 480

Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile
485 490 495

Arg Ala Val Thr Ile Asn Arg Met Met Ser Tyr Leu Asn Ala Ser
500 505 510

<210> 45
<211> 1533
<212> DNA
<213> Felis catus

<400> 45
ggaaggcatc agatagctca tcattctatt gatggtaact gcacgaattc tgaaagcatg 60
aagaagtatg cagagcttga ttttagttt ataaaaatcc gggtcttcca aggaggagtt 120
ctgtggcaca gtcacactgt tgacattcag ggcctgtaac agctcatcaa tagctgtcag 180
catgtttga tccagaaaaga tctgcctttt aggatccatt aacagcttg cattcatggc 240
cttgaactcc acctggtaca tcttcaagtc ctcatagata ctgctaaggc acagggtcgt 300
cataaaagag gtctttctgg aggccaggca actcccatta gttatcagag agatctct 360
ggaagccagg caactctcat tcatggtaa ttccagtggt aagcaggcct ccactgtgct 420
ggttttatct tttgtgatat ctcatgatc aatctttcg gaagtgcagg agtaaaattc 480
tagagtttgt ctggccttct gaagcgtgtt gctgatggct cgacgcaggg tttgggagtg 540

gttggggcac	tggaacatcc	ccggggatgg	agttaggggtt	ggcaagtttc	tagatccgcc	600
gccaccgcca	ccactgcagg	acacggatgc	ccagttgctc	caggatgagc	tatagtagcg	660
gtctctggct	tgcacgcgga	tcttggcattc	cttgtggcac	acgaccttgg	ctgaggtctt	720
gtccacggag	agtctgtctt	tctttctct	gttgttcttg	ccctggacct	gtacgccaaa	780
tgttaaggag	aagtaggaat	gtggggtgct	ccaggtgtca	gggtattccc	agctcacttc	840
cacatgccga	gaattttta	atggcttcag	ttgcaggttc	ttgggtgggt	ccgggttgat	900
gatgtccctg	atgaagaagc	tgctggtgta	gtttcgtac	ttgagcttgt	aatagcgtc	960
caccacgact	tcaatggta	ggctctcctc	ggcagccggg	caggcactgc	cctcctgaca	1020
ctccactgt	tacttcttat	aatccctgtt	gtccactctg	accttctctg	ctgagagtgt	1080
cgctgctcca	caagtcacct	cttgggggtc	agaggagcct	ctgctgcttt	tgacagtgaa	1140
tttcaaatacg	gtactgattt	ccgtcagccca	ccagcaggtg	aaacgtccag	aataattctt	1200
tgccctcacat	tttagaaaaga	tcttattttt	ggatttttc	tgttccctta	agatatcagt	1260
ggaccaaatt	ccatcttcct	tttgtgtat	caggaggaac	aatggctca	gaacctcgcc	1320
tcctttatga	caggtatact	ggccagcatc	tgcaaattct	ttgacttgga	tggtcagagt	1380
tttaccagag	cctaggactt	cactgctctg	gtcagaggc	caggtgatgt	catcttcctc	1440
aggagtattt	caggtgagga	ccaccatttc	tccggggca	tcagggtgcc	agtccaaactc	1500
tacaacataa	acgaaaaat	ccagttccca	tat			1533

<210> 46
 <211> 666
 <212> DNA
 <213> Canis familiaris

<220>	
<221>	CDS
<222>	(1)..(666)
<400>	46
atg tgc ccg ccg cgc ggc ctc ctc ctt gtg acc atc ctg gtc ctg cta	48
Met Cys Pro Pro Arg Gly Leu Leu Leu Val Thr Ile Leu Val Leu Leu	
1 5 10 15	
agc cac ctg gac cac ctt act tgg gcc agg agc ctc ccc aca gcc tca	96
Ser His Leu Asp His Leu Thr Trp Ala Arg Ser Leu Pro Thr Ala Ser	
20 25 30	
ccg agc cca gga ata ttc cag tgc ctc aac cac tcc caa aac ctg ctg	144
Pro Ser Pro Gly Ile Phe Gln Cys Leu Asn His Ser Gln Asn Leu Leu	
35 40 45	

aga gcc gtc agc aac acg ctt cag aag gcc aga caa act cta gaa tta		192
Arg Ala Val Ser Asn Thr Leu Gln Lys Ala Arg Gln Thr Leu Glu Leu		
50 55 60		
tat tcc tgc act tcc gaa gag att gat cat gaa gat atc aca aag gat		240
Tyr Ser Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp		
65 70 75 80		
aaa acc agc aca gtg gag gcc tgc tta cca ctg gaa tta acc atg aat		288
Lys Thr Ser Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Met Asn		
85 90 95		
gag agt tgc ctg gct tcc aga gag atc tct ttg ata act aac ggg agt		336
Glu Ser Cys Leu Ala Ser Arg Glu Ile Ser Leu Ile Thr Asn Gly Ser		
100 105 110		
tgc ctg gcc tct gga aag gcc tct ttt atg acg gtc ctg tgc ctt agc		384
Cys Leu Ala Ser Gly Lys Ala Ser Phe Met Thr Val Leu Cys Leu Ser		
115 120 125		
agc atc tat gag gac ttg aag atg tac cag atg gaa ttc aag gcc atg		432
Ser Ile Tyr Glu Asp Leu Lys Met Tyr Gln Met Glu Phe Lys Ala Met		
130 135 140		
aac gca aag ctt tta atg gat ccc aag agg cag atc ttt ctg gat caa		480
Asn Ala Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln		
145 150 155 160		
aac atg ctg aca gct atc gat gag ctg tta cag gcc ctg aat ttc aac		528
Asn Met Leu Thr Ala Ile Asp Glu Leu Gln Ala Leu Asn Phe Asn		
165 170 175		
agt gtg act gtg cca cag aaa tcc tcc ctt gaa gag ccg gat ttt tat		576
Ser Val Thr Val Pro Gln Lys Ser Ser Leu Glu Glu Pro Asp Phe Tyr		
180 185 190		
aaa act aaa atc aag ctc tgc ata ctt ctt cat gct ttc aga att cgt		624
Lys Thr Lys Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg		
195 200 205		
gcg gtg acc atc gat aga atg atg agt tat ctg aat tct tcc		666
Ala Val Thr Ile Asp Arg Met Met Ser Tyr Leu Asn Ser Ser		
210 215 220		

<210> 47
<211> 222
<212> PRT
<213> Canis familiaris

<400> 47

Met Cys Pro Pro Arg Gly Leu Leu Leu Val Thr Ile Leu Val Leu Leu		
1 5 10 15		

Ser His Leu Asp His Leu Thr Trp Ala Arg Ser Leu Pro Thr Ala Ser
20 25 30

Pro Ser Pro Gly Ile Phe Gln Cys Leu Asn His Ser Gln Asn Leu Leu
35 40 45

Arg Ala Val Ser Asn Thr Leu Gln Lys Ala Arg Gln Thr Leu Glu Leu
50 55 60

Tyr Ser Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp
65 70 75 80

Lys Thr Ser Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Met Asn
85 90 95

Glu Ser Cys Leu Ala Ser Arg Glu Ile Ser Leu Ile Thr Asn Gly Ser
100 105 110

Cys Leu Ala Ser Gly Lys Ala Ser Phe Met Thr Val Leu Cys Leu Ser
115 120 125

Ser Ile Tyr Glu Asp Leu Lys Met Tyr Gln Met Glu Phe Lys Ala Met
130 135 140

Asn Ala Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln
145 150 155 160

Asn Met Leu Thr Ala Ile Asp Glu Leu Leu Gln Ala Leu Asn Phe Asn
165 170 175

Ser Val Thr Val Pro Gln Lys Ser Ser Leu Glu Glu Pro Asp Phe Tyr
180 185 190

Lys Thr Lys Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg
195 200 205

Ala Val Thr Ile Asp Arg Met Met Ser Tyr Leu Asn Ser Ser
210 215 220

<210> 48
<211> 666
<212> DNA
<213> Canis familiaris

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aagaagtatg cagagcttga ttttagttt ataaaaatcc ggctttcaa gggaggattt	120
ctgtggcaca gtcacactgt taaaattcag ggcctgtaac agctcatcga tagctgtcag	180
catgttttga tccagaaaaga tctgcctctt gggatccatt aaaagcttg cgttcatggc	240
cttgaattcc atctggtaca tcttcaagtc ctcatagatg ctgctaaggc acaggaccgt	300
cataaaagag gcctttccag aggccaggca actccgtta gttatcaaag agatctct	360
ggaagccagg caactctcat tcatggtaa ttccagtgg aagcaggcct ccactgtgct	420
ggtttatcc tttgtgatat ctcatgatc aatctttcg gaagtgcagg aatataattc	480
tagagtttgt ctggccttct gaagcgtgtt gctgacggct ctcagcaggt tttggagtg	540
gttgaggcac tggaaatattc ctgggctcgg tgaggctgtg gggaggctcc tggcccaagt	600
aaggtggtcc aggtggctta gcaggaccag gatggtcaca aggaggaggc cgcgccggcgg	660
gcacat	666

<210>	49
<211>	591
<212>	DNA
<213>	Canis familiaris

<220>	
<221>	CDS
<222>	(1)...(591)

<400>	49
agg agc ctc ccc aca gcc tca ccg agc cca gga ata ttc cag tgc ctc	48
Arg Ser Leu Pro Thr Ala Ser Pro Ser Pro Gly Ile Phe Gln Cys Leu	
1 5 10 15	
aac cac tcc caa aac ctg ctg aga gcc gtc agc aac acg ctt cag aag	96
Asn His Ser Gln Asn Leu Leu Arg Ala Val Ser Asn Thr Leu Gln Lys	
20 25 30	
gcc aga caa act cta gaa tta tat tcc tgc act tcc gaa gag att gat	144
Ala Arg Gln Thr Leu Glu Leu Tyr Ser Cys Thr Ser Glu Glu Ile Asp	
35 40 45	
cat gaa gat atc aca aag gat aaa acc agc aca gtg gag gcc tgc tta	192
His Glu Asp Ile Thr Lys Asp Lys Thr Ser Thr Val Glu Ala Cys Leu	
50 55 60	
cca ctg gaa tta acc atg aat gag agt tgc ctg gct tcc aga gag atc	240
Pro Leu Glu Leu Thr Met Asn Glu Ser Cys Leu Ala Ser Arg Glu Ile	
65 70 75 80	

tct ttg ata act aac ggg agt tgc ctg gcc tct gga aag gcc tct ttt Ser Leu Ile Thr Asn Gly Ser Cys Leu Ala Ser Gly Lys Ala Ser Phe	85	90	95	288	
atg acg gtc ctg tgc ctt agc agc atc tat gag gac ttg aag atg tac Met Thr Val Leu Cys Leu Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr	100	105	110	336	
cag atg gaa ttc aag gcc atg aac gca aag ctt tta atg gat ccc aag Gln Met Glu Phe Lys Ala Met Asn Ala Lys Leu Leu Met Asp Pro Lys	115	120	125	384	
agg cag atc ttt ctg gat caa aac atg ctg aca gct atc gat gag ctg Arg Gln Ile Phe Leu Asp Gln Asn Met Leu Thr Ala Ile Asp Glu Leu	130	135	140	432	
tta cag gcc ctg aat ttc aac agt gtg act gtg cca cag aaa tcc tcc Leu Gln Ala Leu Asn Phe Asn Ser Val Thr Val Pro Gln Lys Ser Ser	145	150	155	160	480
ctt gaa gag ccg gat ttt tat aaa act aaa atc aag ctc tgc ata ctt Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu	165	170	175	528	
ctt cat gct ttc aga att cgt gcg gtg acc atc gat aga atg atg agt Leu His Ala Phe Arg Ile Arg Ala Val Thr Ile Asp Arg Met Met Ser	180	185	190	576	
tat ctg aat tct tcc Tyr Leu Asn Ser Ser	195			591	

<210> 50
<211> 197
<212> PRT
<213> Canis familiaris

<400> 50

Arg Ser Leu Pro Thr Ala Ser Pro Ser Pro Gly Ile Phe Gln Cys Leu
1 5 10 15

Asn His Ser Gln Asn Leu Leu Arg Ala Val Ser Asn Thr Leu Gln Lys
20 25 30

Ala Arg Gln Thr Leu Glu Leu Tyr Ser Cys Thr Ser Glu Glu Ile Asp
35 40 45

His Glu Asp Ile Thr Lys Asp Lys Thr Ser Thr Val Glu Ala Cys Leu
50 55 60

Pro Leu Glu Leu Thr Met Asn Glu Ser Cys Leu Ala Ser Arg Glu Ile

65 70 75 80

Ser Leu Ile Thr Asn Gly Ser Cys Leu Ala Ser Gly Lys Ala Ser Phe
85 90 95

Met Thr Val Leu Cys Leu Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr
 100 105 110

Gln Met Glu Phe Lys Ala Met Asn Ala Lys Leu Leu Met Asp Pro Lys
 115 120 125

Arg Gln Ile Phe Leu Asp Gln Asn Met Leu Thr Ala Ile Asp Glu Leu
130 135 140

Leu Gln Ala Leu Asn Phe Asn Ser Val Thr Val Pro Gln Lys Ser Ser
 145 150 155 160

Leu His Ala Phe Arg Ile Arg Ala Val Thr Ile Asp Arg Met Met Ser
180 185 190

Tyr Leu Asn Ser Ser
195

<210> 51
<211> 591
<212> DNA
<213> *Canis familiaris*

<400> 51
ggaaagaattc agataactca tcattctatc gatggtcacc gcacgaattc taaaaggcatg 60

aagaagtatg cagagcttga ttttagtttt ataaaaaatcc ggcttcaa gggaggattt 120

ctgtggcaca gtcacactgt tgaaattcag ggcctgtaac agctcatcga tagctgtcag 180

catgtttga tccagaaaaga tctgcctctt gggatccatt aaaagctttg cgttcatggc 240

cttgaattcc atctggtaca tcttcaagtc ctcatagatg ctgctaaggc acaggaccgt 300

cataaaagag gccttccag aggccaggca actcccgtta gttatcaaag agatctctct 360

ggaagccagg caactctcat tcatggtaa ttccagtggt aagcaggcct ccactgtgct 420

gggttttatcc tttgtatcat cttcatgatc aatctttcg qaagtgcagg aatataattc 480

tagagttgt ctggccttct gaagcgtgtt gctgacggct ctcagcagg tttgggagtg	540
gttggggcac tggaatattc ctgggctcggt gggaggctcc t	591
<210> 52	
<211> 921	
<212> DNA	
<213> Canis familiaris	
<220>	
<221> CDS	
<222> (1)..(921)	
<400> 52	
ata tgg gaa ctg gag aaa gat gtt tat gtt gta gag ttg gac tgg cac	48
Ile Trp Glu Leu Glu Lys Asp Val Tyr Val Val Glu Leu Asp Trp His	
1 5 10 15	
cct gat gcc ccc gga gaa atg gtg gtc ctc acc tgc cat acc cct gaa	96
Pro Asp Ala Pro Gly Glu Met Val Val Leu Thr Cys His Thr Pro Glu	
20 25 30	
gaa gat gac atc act tgg acc tca gcg cag agc agt gaa gtc cta ggt	144
Glu Asp Asp Ile Thr Trp Thr Ser Ala Gln Ser Ser Glu Val Leu Gly	
35 40 45	
tct ggt aaa act ctg acc atc caa gtc aaa gaa ttt gga gat gct ggc	192
Ser Gly Lys Thr Leu Thr Ile Gln Val Lys Glu Phe Gly Asp Ala Gly	
50 55 60	
cag tat acc tgc cat aaa gga ggc aag gtt ctg agc cgc tca ctc ctg	240
Gln Tyr Thr Cys His Lys Gly Gly Lys Val Leu Ser Arg Ser Leu Leu	
65 70 75 80	
ttg att cac aaa aaa gaa gat gga att tgg tcc act gat atc tta aag	288
Leu Ile His Lys Lys Glu Asp Gly Ile Trp Ser Thr Asp Ile Leu Lys	
85 90 95	
gaa cag aaa gaa tcc aaa aat aag atc ttt ctg aaa tgt gag gca aag	336
Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe Leu Lys Cys Glu Ala Lys	
100 105 110	
aat tat tct gga cgt ttc aca tgc tgg ctg acg gca atc agt act	384
Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp Leu Thr Ala Ile Ser Thr	
115 120 125	
gat ttg aaa ttc agt gtc aaa agt agc aga ggc ttc tct gac ccc caa	432
Asp Leu Lys Phe Ser Val Lys Ser Ser Arg Gly Phe Ser Asp Pro Gln	
130 135 140	
ggg gtg aca tgt gga gca gtg aca ctt tca gca gag agg gtc aga gtg	480
Gly Val Thr Cys Gly Ala Val Thr Leu Ser Ala Glu Arg Val Arg Val	
145 150 155 160	
gac aac agg gat tat aag aag tac aca gtg gag tgt cag gag ggc agt	528

Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val Glu Cys Gln Glu Gly Ser			
165	170	175	
gcc tgc ccc tct gcc gag gag agc cta ccc atc gag gtc gtg gtg gat			576
Ala Cys Pro Ser Ala Glu Glu Ser Leu Pro Ile Glu Val Val Val Asp			
180	185	190	
gct att cac aag ctc aag tat gaa aac tac acc agc agc ttc ttc atc			624
Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr Thr Ser Ser Phe Phe Ile			
195	200	205	
aga gac atc atc aaa cca gac cca aca aac ctg cag ctg aag cca			672
Arg Asp Ile Ile Lys Pro Asp Pro Pro Thr Asn Leu Gln Leu Lys Pro			
210	215	220	
ttg aaa aat tct cggttggcacgtggatcgatggaaatccgacc			720
Leu Lys Asn Ser Arg His Val Glu Val Ser Trp Glu Tyr Pro Asp Thr			
225	230	235	240
tgg agc acc cca cat tcc tac ttc tcc ctg aca ttt tgc ata cag gcc			768
Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr Phe Cys Ile Gln Ala			
245	250	255	
cag ggc aag aac aat aga gaa aag aaa gat aga ctc tgc gtg gac aag			816
Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp Arg Leu Cys Val Asp Lys			
260	265	270	
acc tca gcc aag gtc gtg tgc cac aag gat gcc aag atc cgc gtg caa			864
Thr Ser Ala Lys Val Val Cys His Lys Asp Ala Lys Ile Arg Val Gln			
275	280	285	
gcc cga gac cgc tac tat agt tca tcc tgg agc gac tgg gca tct gtg			912
Ala Arg Asp Arg Tyr Tyr Ser Ser Trp Ser Asp Trp Ala Ser Val			
290	295	300	
tcc tgc agt			921
Ser Cys Ser			
305			
<210> 53			
<211> 307			
<212> PRT			
<213> Canis familiaris			
<400> 53			
Ile Trp Glu Leu Glu Lys Asp Val Tyr Val Val Glu Leu Asp Trp His			
1	5	10	15
Pro Asp Ala Pro Gly Glu Met Val Val Leu Thr Cys His Thr Pro Glu			
20	25	30	
Glu Asp Asp Ile Thr Trp Thr Ser Ala Gln Ser Ser Glu Val Leu Gly			
35	40	45	

Ser Gly Lys Thr Leu Thr Ile Gln Val Lys Glu Phe Gly Asp Ala Gly
50 55 60

Gln Tyr Thr Cys His Lys Gly Gly Lys Val Leu Ser Arg Ser Leu Leu
65 70 75 80

Leu Ile His Lys Lys Glu Asp Gly Ile Trp Ser Thr Asp Ile Leu Lys
85 90 95

Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe Leu Lys Cys Glu Ala Lys
100 105 110

Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp Leu Thr Ala Ile Ser Thr
115 120 125

Asp Leu Lys Phe Ser Val Lys Ser Ser Arg Gly Phe Ser Asp Pro Gln
130 135 140

Gly Val Thr Cys Gly Ala Val Thr Leu Ser Ala Glu Arg Val Arg Val
145 150 155 160

Asp Asn Arg Asp Tyr Lys Tyr Thr Val Glu Cys Gln Glu Gly Ser
165 170 175

Ala Cys Pro Ser Ala Glu Glu Ser Leu Pro Ile Glu Val Val Val Asp
180 185 190

Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr Thr Ser Ser Phe Phe Ile
195 200 205

Arg Asp Ile Ile Lys Pro Asp Pro Pro Thr Asn Leu Gln Leu Lys Pro
210 215 220

Leu Lys Asn Ser Arg His Val Glu Val Ser Trp Glu Tyr Pro Asp Thr
225 230 235 240

Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr Phe Cys Ile Gln Ala
245 250 255

Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp Arg Leu Cys Val Asp Lys
260 265 270

Thr Ser Ala Lys Val Val Cys His Lys Asp Ala Lys Ile Arg Val Gln
275 280 285

Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp Ser Asp Trp Ala Ser Val
290 295 300

Ser Cys Ser
305

<210> 54
<211> 921
<212> DNA
<213> *Canis familiaris*

<400> 54
actgcaggac acagatgccc agtcgctcca ggatgaacta tagtagcggt ctcgggcttg 60
cacgcggatc ttggcatcct tgtggcacac gaccttggt gaggtcttgt ccacgcagag 120
tctatcttc ttttctctat tgttcttgcc ctgggcctgt atgcaaaatg tcagggagaa 180
gtaggaatgt ggggtgctcc aggtgtcggg gtattccag ctgacctcca cgtgccgaga 240
atttttcaat ggcttcagct gcaggtttgt gggtggtct ggtttcatgtat tgctctgtat 300
gaagaagctg ctgggttagt tttcatactt gagcttgtga atagcatcca ccacgacactc 360
gatgggttagg ctctcctcgg cagagggca ggcactgccc tcctgacact ccactgtgtat 420
cttcttataa tccctgttgtt ccactctgac cctctctgt gaaagtgtca ctgctccaca 480
tgtcacccct tgggggtcag agaaggctct gctacttttgc acactgaatt tcaaatacgat 540
actgattgcc gtcagccacc agcatgtgaa acgtccagaa taattcttgc cctcacattt 600
cagaaagatc ttatTTTgg attctttctg tcccttaag atatcagtgg accaaattcc 660
atcttctttt ttgtaatca acaggagtga gcggtcaga accttgcctc ctttatggca 720
ggtataactgg ccagcatctc caaattctt gacttggatg gtcagatgtt taccagaacc 780
taggacttca ctgctctgatg ctgaggatcca agtcatgtca tcttcttcag gggatggca 840
ggtgaggacc accatttctc cggggcatc agggtgccag tccaaactcta caacataaac 900
atctttctcc agttccccata t 921

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<210> 55
<211> 985
<212> DNA
<213> Felis catus
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<220>
 <221> CDS
 <222> (1)..(984)

<400> 55		
atg cat cct cag cag ttg gtc atc gcc tgg ttt tcc ctg gtt ttg ctg		48
Met His Pro Gln Gln Leu Val Ile Ala Trp Phe Ser Leu Val Leu Leu		
1 5 10 15		
gca cct ccc ctc atg gcc ata tgg gaa ctg gag aaa aac gtt tat gtt		96
Ala Pro Pro Leu Met Ala Ile Trp Glu Leu Glu Lys Asn Val Tyr Val		
20 25 30		
gta gag ttg gac tgg cac cct gat gcc ccc gga gaa atg gtg gtc ctc		144
Val Glu Leu Asp Trp His Pro Asp Ala Pro Gly Glu Met Val Val Leu		
35 40 45		
acc tgc aat act cct gaa gaa gat gac atc acc tgg acc tct gac cag		192
Thr Cys Asn Thr Pro Glu Asp Asp Ile Thr Trp Thr Ser Asp Gln		
50 55 60		
agc agt gaa gtc cta ggc tct ggt aaa act ctg acc atc caa gtc aaa		240
Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys		
65 70 75 80		
gaa ttt gca gat gct ggc cag tat acc tgt cat aaa gga ggc gag gtt		288
Glu Phe Ala Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu Val		
85 90 95		
ctg agc cat tcg ttc ctc ctg ata cac aaa aag gaa gat gga att tgg		336
Leu Ser His Ser Phe Leu Leu Ile His Lys Lys Glu Asp Gly Ile Trp		
100 105 110		
tcc act gat atc tta agg gaa cag aaa gaa tcc aaa aat aag atc ttt		384
Ser Thr Asp Ile Leu Arg Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe		
115 120 125		
cta aaa tgt gag gca aag aat tat tct gga cgt ttc acc tgc tgg tgg		432
Leu Lys Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp		
130 135 140		
ctg acg gca atc agt acc gat ttg aaa ttc act gtc aaa agc agc aga		480
Leu Thr Ala Ile Ser Thr Asp Leu Lys Phe Thr Val Lys Ser Ser Arg		
145 150 155 160		
ggc tcc tct gac ccc caa ggg gtg act tgt gga gca gcg aca ctc tca		528
Gly Ser Ser Asp Pro Gln Gly Val Thr Cys Gly Ala Ala Thr Leu Ser		
165 170 175		
gca gag aag gtc aga gtg gac aac agg gat tat aag aag tac aca gtg		576
Ala Glu Lys Val Arg Val Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val		
180 185 190		
gag tgt cag gag ggc agt gcc tgc ccg gct gcc gag gag agc cta ccc		624
Glu Cys Gln Glu Gly Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro		
195 200 205		

att gaa gtc gtg gtg gac gct att cac aag ctc aag tac gaa aac tac Ile Glu Val Val Val Asp Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr 210	215	220	672
acc agc agc ttc ttc atc agg gac atc atc aaa ccg gac cca ccc aag Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys 225	230	235	720
aac ctg caa ctg aag cca tta aaa aat tct cggttcatgtgaaatgttgg Asn Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg His Val Glu Val Ser 245	250	255	768
tgg gaa tac cct gac acc tgg agc acc cca cat tcc tac ttc tcc tta Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu 260	265	270	816
aca ttt ggc gta cag gtc cag ggc aag aac aac aga gaa aag aaa gac Thr Phe Gly Val Gln Val Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp 275	280	285	864
aga ctc tcc gtg gac aag acc tca gcc aag gtc gtg tgc cac aag gat Arg Leu Ser Val Asp Lys Thr Ser Ala Lys Val Val Cys His Lys Asp 290	295	300	912
gcc aag atc cgc gtg caa gcc aga gac cgc tac tat agc tca tcc tgg Ala Lys Ile Arg Val Gln Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp 305	310	315	960
agc aac tgg gca tcc gtg tcc tgc a Ser Asn Trp Ala Ser Val Ser Cys 325			985

<210> 56
<211> 328
<212> PRT
<213> *Felis catus*

5400> 56

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Met His Pro Gln Gln Leu Val Ile Ala Trp Phe Ser Leu Val Leu Leu
1           5           10          15

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Ala Pro Pro Leu Met Ala Ile Trp Glu Leu Glu Lys Asn Val Tyr Val
20 25 30

Val Glu Leu Asp Trp His Pro Asp Ala Pro Gly Glu Met Val Val Leu
35 40 45

Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys
65 70 75 80

Glu Phe Ala Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu Val
85 90 95

Leu Ser His Ser Phe Leu Leu Ile His Lys Lys Glu Asp Gly Ile Trp
100 105 110

Ser Thr Asp Ile Leu Arg Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe
115 120 125

Leu Lys Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp
130 135 140

Leu Thr Ala Ile Ser Thr Asp Leu Lys Phe Thr Val Lys Ser Ser Arg
145 150 155 160

Gly Ser Ser Asp Pro Gln Gly Val Thr Cys Gly Ala Ala Thr Leu Ser
165 170 175

Ala Glu Lys Val Arg Val Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val
180 185 190

Glu Cys Gln Glu Gly Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro
195 200 205

Ile Glu Val Val Asp Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr
210 215 220

Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys
225 230 235 240

Asn Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg His Val Glu Val Ser
245 250 255

Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu
260 265 270

Thr Phe Gly Val Gln Val Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp
275 280 285

Arg Leu Ser Val Asp Lys Thr Ser Ala Lys Val Val Cys His Lys Asp

290

295

300

Ala Lys Ile Arg Val Gln Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp
305 310 315 320

Ser Asn Trp Ala Ser Val Ser Cys
325

<210> 57
<211> 985
<212> DNA
<213> Felis catus

<400> 57
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tgtctttctt ttctctgttg ttcttgccct ggacctgtac gccaaatgtt aaggagaagt 180
aggaatgtgg ggtgctccag gtgtcagggt attccagct cacttccaca tgccgagaat 240
tttttaatgg cttcagttgc agttcttggt gtgggtccgg tttgatgtatg tccctgtatga 300
agaagctgct ggtgttagtt tcgtacttga gcttgtgaat agcgtccacc acgacttcaa 360
tgggtaggct ctcctcggca gccgggcagg cactgccctc ctgacactcc actgtgtact 420
tcttataatc cctgttgtcc actctgaccc tctctgtga gagtgtcgt gctccacaag 480
tcaccccttg ggggtcagag gagcctctgc tgctttgac agtgaatttc aaatcggtac 540
tgattgccgt cagccaccag caggtgaaac gtccagaata attcttgcc tcacatTTA 600
gaaagatctt atttttggat tctttctgtt cccttaagat atcagtggac caaattccat 660
cttcctttt gtgtatcagg aggaacgaat ggctcagaac ctcgcctcct ttatgacagg 720
tatactggcc agcatctgca aattcttga cttggatggc cagagttta ccagagccta 780
ggacttcact gctctggta gaggtccagg tgatgtcatc ttcttcagga gtattgcagg 840
tgaggaccac catttctccg ggggcatcag ggtgccagtc caactctaca acataaacgt 900
ttttctccag ttccccatatg gccatgaggg gaggtgccag caaaaaccagg gaaaaaccagg 960
cgatgaccaa ctgctgagga tgcatt 985

<210> 58
<211> 987
<212> DNA
<213> Canis familiaris

<220>
 <221> CDS
 <222> (1)...(987)

<400>	58		
atg cac cct cag cag ttg gtc atc tcc tgg ttt tcc ctc gtt ttg ctg		48	
Met His Pro Gln Gln Leu Val Ile Ser Trp Phe Ser Leu Val Leu Leu			
1	5	10	15
gcg tct ccc ctc atg gcc ata tgg gaa ctg gag aaa gat gtt tat gtt		96	
Ala Ser Pro Leu Met Ala Ile Trp Glu Leu Glu Lys Asp Val Tyr Val			
20	25	30	
gta gag ttg gac tgg cac cct gat gcc ccc gga gaa atg gtg gtc ctc		144	
Val Glu Leu Asp Trp His Pro Asp Ala Pro Gly Glu Met Val Val Leu			
35	40	45	
acc tgc cat acc cct gaa gaa gat gac atc act tgg acc tca gcg cag		192	
Thr Cys His Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser Ala Gln			
50	55	60	
agc agt gaa gtc cta ggt tct ggt aaa act ctg acc atc caa gtc aaa		240	
Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys			
65	70	75	80
gaa ttt gga gat gct ggc cag tat acc tgc cat aaa gga ggc aag gtt		288	
Glu Phe Gly Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Lys Val			
85	90	95	
ctg agc cgc tca ctc ctg ttg att cac aaa aaa gaa gat gga att tgg		336	
Leu Ser Arg Ser Leu Leu Ile His Lys Lys Glu Asp Gly Ile Trp			
100	105	110	
tcc act gat atc tta aag gaa cag aaa gaa tcc aaa aat aag atc ttt		384	
Ser Thr Asp Ile Leu Lys Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe			
115	120	125	
ctg aaa tgt gag gca aag aat tat tct gga cgt ttc aca tgc tgg tgg		432	
Leu Lys Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp			
130	135	140	
ctg acg gca atc agt act gat ttg aaa ttc agt gtc aaa agt agc aga		480	
Leu Thr Ala Ile Ser Thr Asp Leu Lys Phe Ser Val Lys Ser Ser Arg			
145	150	155	160
ggc ttc tct gac ccc caa ggg gtg aca tgt gga gca gtg aca ctt tca		528	
Gly Phe Ser Asp Pro Gln Gly Val Thr Cys Gly Ala Val Thr Leu Ser			
165	170	175	
gca gag agg gtc aga gtg gac aac agg gat tat aag aag tac aca gtg		576	
Ala Glu Arg Val Arg Val Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val			
180	185	190	
gag tgt cag gag ggc agt gcc tgc ccc tct gcc gag gag agc cta ccc		624	
Glu Cys Gln Glu Gly Ser Ala Cys Pro Ser Ala Glu Glu Ser Leu Pro			
195	200	205	

atc gag gtc gtg gtg gat att cac aag ctc aag tat gaa aac tac Ile Glu Val Val Val Asp Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr 210	215	220	672
acc agc agc ttc ttc atc aga gac atc atc aaa cca gac cca ccc aca Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Thr 225	230	235	240
aac ctg cag ctg aag cca ttg aaa aat tct cggttggcacgttgaggtcagc Asn Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg His Val Glu Val Ser 245	250	255	768
tgg gaa tac ccc gac acc tgg agc acc cca cat tcc tac ttc tcc ctg Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu 260	265	270	816
aca ttt tgc ata cag gcc cag ggc aag aac aat aga gaa aag aaa gat Thr Phe Cys Ile Gln Ala Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp 275	280	285	864
aga ctc tgc gtg gac aag acc tca gcc aag gtc gtg tgc cac aag gat Arg Leu Cys Val Asp Lys Thr Ser Ala Lys Val Val Cys His Lys Asp 290	295	300	912
gcc aag atc cgc gtg caa gcc cga gac cgc tac tat agt tca tcc tgg Ala Lys Ile Arg Val Gln Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp 305	310	315	960
agt gac tgg gca tct gtg tca tgc agt Ser Asp Trp Ala Ser Val Ser Cys Ser 325			987

<210> 59
<211> 329
<212> PRT
<213> Canis familiaris

<400> 59

Met	His	Pro	Gln	Gln	Leu	Val	Ile	Ser	Trp	Phe	Ser	Leu	Val	Leu	Leu
1				5					10					15	

Ala Ser Pro Leu Met Ala Ile Trp Glu Leu Glu Lys Asp Val Tyr Val
20 25 30

Val Glu Leu Asp Trp His Pro Asp Ala Pro Gly Glu Met Val Val Leu
35 40 45

Thr Cys His Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser Ala Gln
50 55 60

Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys
65 70 75 80

Glu Phe Gly Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Lys Val
85 90 95

Leu Ser Arg Ser Leu Leu Leu Ile His Lys Lys Glu Asp Gly Ile Trp
100 105 110

Ser Thr Asp Ile Leu Lys Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe
115 120 125

Leu Lys Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp
130 135 140

Leu Thr Ala Ile Ser Thr Asp Leu Lys Phe Ser Val Lys Ser Ser Arg
145 150 155 160

Gly Phe Ser Asp Pro Gln Gly Val Thr Cys Gly Ala Val Thr Leu Ser
165 170 175

Ala Glu Arg Val Arg Val Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val
180 185 190

Glu Cys Gln Glu Gly Ser Ala Cys Pro Ser Ala Glu Glu Ser Leu Pro
195 200 205

Ile Glu Val Val Asp Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr
210 215 220

Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Thr
225 230 235 240

Asn Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg His Val Glu Val Ser
245 250 255

Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu
260 265 270

Thr Phe Cys Ile Gln Ala Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp
275 280 285

Arg Leu Cys Val Asp Lys Thr Ser Ala Lys Val Val Cys His Lys Asp

290

295

300

Ala Lys Ile Arg Val Gln Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp
305 310 315 320

Ser Asp Trp Ala Ser Val Ser Cys Ser
325

<210> 60
<211> 987
<212> DNA
<213> Canis familiaris

<400> 60
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cacgcggatc ttggcatcct tgtggcacac gaccttggct gaggtcttgtt ccacgcagag 120
tctatctttc ttttctctat ttttcttgcc ctggggctgt atgcaaaatg tcagggagaa 180
gttaggaatgt ggggtgtcc aggtgtcggg gtattccag ctgacacctca cgtgccgaga 240
attttcaat ggcttcagct gcagggttgtt ggggtgggtct ggtttgatga tgtctctgat 300
gaagaagctg ctgggttagt tttcatactt gagcttgtga atagcatcca ccacgacactc 360
gatgggttagg ctctccctcg cagaggggca ggcactgccc tcctgacact ccactgtgta 420
cttcttataa tccctgttgtt ccactctgac cctcttgct gaaagtgtca ctgctccaca 480
tgtcaccctt tgggggtcag agaaggctct gctactttt acactgaatt tcaaatacgat 540
actgattgcc gtcagccacc agcatgtgaa acgtccagaa taattcttg cctcacattt 600
cagaaagatc ttatTTTGG attcttctg ttccttaag atatcagtgg accaaattcc 660
atcttctttt ttgtgaatca acaggagtga gcggctcaga accttgccctc ctatggca 720
ggtataactgg ccagcatctc caaattctt gacttggatg gtcagagttt taccagaacc 780
taggacttca ctgctctgctg ctgaggtcca agtgatgtca tcttctttag gggatggca 840
ggtgaggacc accatttctc cggggccatc agggtgccag tccaaactcta caacataaac 900
atcttctcc agttccata tggccatgag gggagacgcc agcaaaacga gggaaaacca 960
ggagatgacc aactgctgag ggtgcatt 987

<210> 61
<211> 1599
<212> DNA
<213> Canis familiaris

<220>
<221> CDS
<222> (1)...(1599)

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atg cac cct cag cag ttg gtc atc tcc tgg ttt tcc ctc gtt ttg ctg		48
Met His Pro Gln Gln Leu Val Ile Ser Trp Phe Ser Leu Val Leu Leu		
1 5 10 15		
gcg tct ccc ctc atg gcc ata tgg gaa ctg gag aaa gat gtt tat gtt		96
Ala Ser Pro Leu Met Ala Ile Trp Glu Leu Glu Lys Asp Val Tyr Val		
20 25 30		
gta gag ttg gac tgg cac cct gat gcc ccc gga gaa atg gtg gtc ctc		144
Val Glu Leu Asp Trp His Pro Asp Ala Pro Gly Glu Met Val Val Leu		
35 40 45		
acc tgc cat acc cct gaa gaa gat gac atc act tgg acc tca gcg cag		192
Thr Cys His Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser Ala Gln		
50 55 60		
agc agt gaa gtc cta ggt tct ggt aaa act ctg acc atc caa gtc aaa		240
Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys		
65 70 75 80		
gaa ttt gga gat gct ggc cag tat acc tgc cat aaa gga ggc aag gtt		288
Glu Phe Gly Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Lys Val		
85 90 95		
ctg agc cgc tca ctc ctg ttg att cac aaa aaa gaa gat gga att tgg		336
Leu Ser Arg Ser Leu Leu Ile His Lys Lys Glu Asp Gly Ile Trp		
100 105 110		
tcc act gat atc tta aag gaa cag aaa gaa tcc aaa aat aag atc ttt		384
Ser Thr Asp Ile Leu Lys Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe		
115 120 125		
ctg aaa tgt gag gca aag aat tat tct gga cgt ttc aca tgc tgg tgg		432
Leu Lys Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp		
130 135 140		
ctg acg gca atc agt act gat ttg aaa ttc agt gtc aaa agt agc aga		480
Leu Thr Ala Ile Ser Thr Asp Leu Lys Phe Ser Val Lys Ser Ser Arg		
145 150 155 160		
ggc ttc tct gac ccc caa ggg gtg aca tgt gga gca gtg aca ctt tca		528
Gly Phe Ser Asp Pro Gln Gly Val Thr Cys Gly Ala Val Thr Leu Ser		
165 170 175		
gca gag agg gtc aga gtg gac aac agg gat tat aag aag tac aca gtg		576
Ala Glu Arg Val Arg Val Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val		
180 185 190		
gag tgt cag gag ggc agt gcc tgc ccc tct gcc gag gag agc cta ccc		624
Glu Cys Gln Glu Gly Ser Ala Cys Pro Ser Ala Glu Glu Ser Leu Pro		
195 200 205		

atc gag gtc gtg gat gct att cac aag ctc aag tat gaa aac tac Ile Glu Val Val Val Asp Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr	672
210 215 220	
acc agc agc ttc ttc atc aga gac atc atc aaa cca gac cca ccc aca Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Thr	720
225 230 235 240	
aac ctg cag ctg aag cca ttg aaa aat tct cggt cac gtg gag gtc agc Asn Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg His Val Glu Val Ser	768
245 250 255	
tgg gaa tac ccc gac acc tgg agc acc cca cat tcc tac ttc tcc ctg Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu	816
260 265 270	
aca ttt tgc ata cag gcc cag ggc aag aac aat aga gaa aag aaa gat Thr Phe Cys Ile Gln Ala Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp	864
275 280 285	
aga ctc tgc gtg gac aag acc tca gcc aag gtc gtg tgc cac aag gat Arg Leu Cys Val Asp Lys Thr Ser Ala Lys Val Val Cys His Lys Asp	912
290 295 300	
gcc aag atc cgc gtg caa gcc cga gac cgc tac tat agt tca tcc tgg Ala Lys Ile Arg Val Gln Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp	960
305 310 315 320	
agc gac tgg gca tct gtg tca tgc agt ggt ggc ggt ggc ggc gga tct Ser Asp Trp Ala Ser Val Ser Cys Ser Gly Gly Gly Gly Gly Ser	1008
325 330 335	
aga aac ttg cca acc cct act cca tcc ccg ggt atg ttc caa tgt ttg Arg Asn Leu Pro Thr Pro Ser Pro Gly Met Phe Gln Cys Leu	1056
340 345 350	
aac cac tcc caa acc ttg ttg aga gcc gtc agc aac acg ctt cag aag Asn His Ser Gln Thr Leu Leu Arg Ala Val Ser Asn Thr Leu Gln Lys	1104
355 360 365	
gcc aga caa act cta gaa tta tat tcc tgc act tcc gaa gag att gat Ala Arg Gln Thr Leu Glu Leu Tyr Ser Cys Thr Ser Glu Glu Ile Asp	1152
370 375 380	
cat gaa gat atc aca aag gat aaa acc agc aca gtg gag gcc tgc tta His Glu Asp Ile Thr Lys Asp Lys Thr Ser Thr Val Glu Ala Cys Leu	1200
385 390 395 400	
cca ctg gaa tta acc atg aat gag agt tgc ctg gct tcc aga gag atc Pro Leu Glu Leu Thr Met Asn Glu Ser Cys Leu Ala Ser Arg Glu Ile	1248
405 410 415	
tct ttg ata act aac ggg agt tgc ctg gcc tct gga aag gcc tct ttt Ser Leu Ile Thr Asn Gly Ser Cys Leu Ala Ser Gly Lys Ala Ser Phe	1296
420 425 430	

atg acg gtc ctg tgc ctt agc agc atc tat gag gac ttg aag atg tac 1344
Met Thr Val Leu Cys Leu Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr
435 440 445

cag atg gaa ttc aag gcc atg aac gca aag ctt tta atg gat ccc aag 1392
Gln Met Glu Phe Lys Ala Met Asn Ala Lys Leu Leu Met Asp Pro Lys
450 455 460

agg cag atc ttt ctg gat caa aac atg ctg aca gct atc gat gag ctg 1440
Arg Gln Ile Phe Leu Asp Gln Asn Met Leu Thr Ala Ile Asp Glu Leu
465 470 475 480

tta cag gcc ctg aat ttc aac agt gtg act gtg cca cag aaa tcc tcc 1488
Leu Gln Ala Leu Asn Phe Asn Ser Val Thr Val Pro Gln Lys Ser Ser
485 490 495

ctt gaa gag ccg gat ttt tat aaa act aaa atc aag ctc tgc ata ctt 1536
Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu
500 505 510

ctt cat gct ttc aga att cgt gcg gtg acc atc aat aga atg atg tcc 1584
Leu His Ala Phe Arg Ile Arg Ala Val Thr Ile Asn Arg Met Met Ser
515 520 525

tac ttg aac tct tcc 1599
Tyr Leu Asn Ser Ser
530

<210> 62
<211> 533
<212> PRT
<213> Canis familiaris

<400> 62

Met His Pro Gln Gln Leu Val Ile Ser Trp Phe Ser Leu Val Leu Leu
1 5 10 15

Ala Ser Pro Leu Met Ala Ile Trp Glu Leu Glu Lys Asp Val Tyr Val
20 25 30

Val Glu Leu Asp Trp His Pro Asp Ala Pro Gly Glu Met Val Val Leu
35 40 45

Thr Cys His Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser Ala Gln
50 55 60

Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys
65 70 75 80

Glu Phe Gly Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Lys Val

85

90

95

Leu Ser Arg Ser Leu Leu Leu Ile His Lys Lys Glu Asp Gly Ile Trp
100 105 110

Ser Thr Asp Ile Leu Lys Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe
115 120 125

Leu Lys Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp
130 135 140

Leu Thr Ala Ile Ser Thr Asp Leu Lys Phe Ser Val Lys Ser Ser Arg
145 150 155 160

Gly Phe Ser Asp Pro Gln Gly Val Thr Cys Gly Ala Val Thr Leu Ser
165 170 175

Ala Glu Arg Val Arg Val Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val
180 185 190

Glu Cys Gln Glu Gly Ser Ala Cys Pro Ser Ala Glu Glu Ser Leu Pro
195 200 205

Ile Glu Val Val Val Asp Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr
210 215 220

Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Thr
225 230 235 240

Asn Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg His Val Glu Val Ser
245 250 255

Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu
260 265 270

Thr Phe Cys Ile Gln Ala Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp
275 280 285

Arg Leu Cys Val Asp Lys Thr Ser Ala Lys Val Val Cys His Lys Asp
290 295 300

Ala Lys Ile Arg Val Gln Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp
305 310 315 320

Ser Asp Trp Ala Ser Val Ser Cys Ser Gly Gly Gly Gly Gly Ser
325 330 335

Arg Asn Leu Pro Thr Pro Thr Pro Ser Pro Gly Met Phe Gln Cys Leu
340 345 350

Asn His Ser Gln Thr Leu Leu Arg Ala Val Ser Asn Thr Leu Gln Lys
355 360 365

Ala Arg Gln Thr Leu Glu Leu Tyr Ser Cys Thr Ser Glu Glu Ile Asp
370 375 380

His Glu Asp Ile Thr Lys Asp Lys Thr Ser Thr Val Glu Ala Cys Leu
385 390 395 400

Pro Leu Glu Leu Thr Met Asn Glu Ser Cys Leu Ala Ser Arg Glu Ile
405 410 415

Ser Leu Ile Thr Asn Gly Ser Cys Leu Ala Ser Gly Lys Ala Ser Phe
420 425 430

Met Thr Val Leu Cys Leu Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr
435 440 445

Gln Met Glu Phe Lys Ala Met Asn Ala Lys Leu Leu Met Asp Pro Lys
450 455 460

Arg Gln Ile Phe Leu Asp Gln Asn Met Leu Thr Ala Ile Asp Glu Leu
465 470 475 480

Leu Gln Ala Leu Asn Phe Asn Ser Val Thr Val Pro Gln Lys Ser Ser
485 490 495

Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu
500 505 510

Leu His Ala Phe Arg Ile Arg Ala Val Thr Ile Asn Arg Met Met Ser
515 520 525

Tyr Leu Asn Ser Ser
530

<210> 63
 <211> 1599
 <212> DNA
 <213> Canis familiaris

<400> 63	
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aagaagtatg cagagcttga ttttagttt ataaaaatcc ggctcttcaa gggaggattt	120
ctgtggcaca gtcacactgt taaaattcag ggcctgtaac agctcatcga tagctgtcag	180
catgtttga tccagaaaaga tctgcctctt gggatccatt aaaagcttg cgttcatggc	240
cttgaattcc atctggtaca tcttcaagtc ctcatagatg ctgctaaggc acaggaccgt	300
cataaaagag gcctttccag aggccaggca actccgtta gttatcaaag agatctct	360
ggaagccagg caactctcat tcatggtaa ttccagtggt aagcaggcct ccactgtgct	420
ggtttatcc tttgtgatat ctcatgatc aatctttcg gaagtgcagg aatataattc	480
tagagtttgt ctggcccttct gaagcgtgtt gctgacggct ctcaacaagg tttggagtg	540
gttcaaacat tggaacatac ccggggatgg agtaggggtt ggcaagttc tagatccgcc	600
gccaccgcca ccactgcatg acacagatgc ccagtcgctc caggatgaac tata>tagcg	660
gtctcgggct tgcacgcgga tcttggcattt cttgtggcac acgaccttgg ctgaggtctt	720
gtccacgcag agtctatctt tctttctctt attgttcttgc ccctggcct gtatgcaaaa	780
tgtcagggag aagtaggaat gtggggtgct ccaggtgtcg gggattccc agctgacctc	840
cacgtgccga gaattttca atggcttcag ctgcaggttt gtgggtgggt ctggtttgat	900
gatgtctctg atgaagaagc tgctggtgta gtttcatac ttgagcttgt gaatagcatc	960
caccacgacc tcgatggta ggctctcctc ggcagagggg caggcactgc ctcctgaca	1020
ctccactgtg tacttcttat aatccctgtt gtccactctg accctctctg ctgaaagtgt	1080
cactgctcca catgtcaccc ctgggggtc agagaaggct ctgctacttt tgacactgaa	1140
tttcaaatac gtactgattt ccgtcagcca ccagcatgtg aaacgtccag aataatttt	1200
tgcctcacat ttcagaaaaga tcttattttt ggatttttc tgttccttta agatatcgt	1260
ggaccaaatt ccatcttctt tttgtgaat caacaggagt gagcggctca gaaccttgcc	1320
tcctttagg caggtatact ggccagcatc tccaaattct ttgacttggta tggtcagagt	1380
tttaccagaa cctaggactt cactgctctg cgctgaggc caagtgtatgt catcttcttc	1440
agggtatgg caggtgagga ccaccatttc tccggggca tcagggtgcc agtccaactc	1500

tacaacataa acatcttct ccagttccca tatggccatg aggggagacg ccagcaaaac	1560
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<400> 64	
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Ile Trp Glu Leu Glu Lys Asp Val Tyr Val Val Glu Leu Asp Trp His	
1 5 10 15	
cct gat gcc ccc gga gaa atg gtg gtc ctc acc tgc cat acc cct gaa	96
Pro Asp Ala Pro Gly Glu Met Val Val Leu Thr Cys His Thr Pro Glu	
20 25 30	
gaa gat gac atc act tgg acc tca gcg cag agc agt gaa gtc cta ggt	144
Glu Asp Asp Ile Thr Trp Thr Ser Ala Gln Ser Ser Glu Val Leu Gly	
35 40 45	
tct ggt aaa act ctg acc atc caa gtc aaa gaa ttt gga gat gct ggc	192
Ser Gly Lys Thr Leu Thr Ile Gln Val Lys Glu Phe Gly Asp Ala Gly	
50 55 60	
cag tat acc tgc cat aaa gga ggc aag gtt ctg agc cgc tca ctc ctg	240
Gln Tyr Thr Cys His Lys Gly Gly Lys Val Leu Ser Arg Ser Leu Leu	
65 70 75 80	
ttg att cac aaa aaa gaa gat gga att tgg tcc act gat atc tta aag	288
Leu Ile His Lys Lys Glu Asp Gly Ile Trp Ser Thr Asp Ile Leu Lys	
85 90 95	
gaa cag aaa gaa tcc aaa aat aag atc ttt ctg aaa tgt gag gca aag	336

Glu	Gln	Lys	Glu	Ser	Lys	Asn	Lys	Ile	Phe	Leu	Lys	Cys	Glu	Ala	Lys	
100								105						110		
aat	tat	tct	gga	cgt	ttc	aca	tgc	tgg	tgg	ctg	acg	gca	atc	agt	act	384
Asn	Tyr	Ser	Gly	Arg	Phe	Thr	Cys	Trp	Trp	Leu	Thr	Ala	Ile	Ser	Thr	
115							120						125			
gat	ttg	aaa	ttc	agt	gtc	aaa	agt	agc	aga	ggc	ttc	tct	gac	ccc	caa	432
Asp	Leu	Lys	Phe	Ser	Val	Lys	Ser	Ser	Arg	Gly	Phe	Ser	Asp	Pro	Gln	
130						135						140				
ggg	gtg	aca	tgt	gga	gca	gtg	aca	ctt	tca	gca	gag	agg	gtc	aga	gtg	480
Gly	Val	Thr	Cys	Gly	Ala	Val	Thr	Leu	Ser	Ala	Glu	Arg	Val	Arg	Val	
145						150					155			160		
gac	aac	agg	gat	tat	aag	aag	tac	aca	gtg	gag	tgt	cag	gag	ggc	agt	528
Asp	Asn	Arg	Asp	Tyr	Lys	Lys	Tyr	Thr	Val	Glu	Cys	Gln	Glu	Gly	Ser	
165							170					175				
gcc	tgc	ccc	tct	gcc	gag	gag	agc	cta	ccc	atc	gag	gtc	gtg	gtg	gat	576
Ala	Cys	Pro	Ser	Ala	Glu	Ser	Leu	Pro	Ile	Glu	Val	Val	Val	Val	Asp	
180							185					190				
gct	att	cac	aag	ctc	aag	tat	gaa	aac	tac	acc	agc	agc	ttc	ttc	atc	624
Ala	Ile	His	Lys	Leu	Lys	Tyr	Glu	Asn	Tyr	Thr	Ser	Ser	Phe	Phe	Ile	
195							200					205				
aga	gac	atc	atc	aaa	cca	gac	cca	ccc	aca	aac	ctg	cag	ctg	aag	cca	672
Arg	Asp	Ile	Ile	Lys	Pro	Asp	Pro	Pro	Thr	Asn	Leu	Gln	Leu	Lys	Pro	
210						215					220					
ttg	aaa	aat	tct	cg	cac	gtg	gag	gtc	agc	tgg	gaa	tac	ccc	gac	acc	720
Leu	Lys	Asn	Ser	Arg	His	Val	Glu	Val	Ser	Trp	Glu	Tyr	Pro	Asp	Thr	
225						230					235			240		
tgg	agc	acc	cca	cat	tcc	tac	ttc	tcc	ctg	aca	ttt	tgc	ata	cag	gcc	768
Trp	Ser	Thr	Pro	His	Ser	Tyr	Phe	Ser	Leu	Thr	Phe	Cys	Ile	Gln	Ala	
245							250					255				
cag	ggc	aag	aac	aat	aga	gaa	aag	aaa	gat	aga	ctc	tgc	gtg	gac	aag	816
Gln	Gly	Lys	Asn	Asn	Arg	Glu	Lys	Lys	Asp	Arg	Leu	Cys	Val	Asp	Lys	
260							265					270				
acc	tca	gcc	aag	gtc	gtg	tgc	cac	aag	gat	gcc	aag	atc	cgc	gtg	caa	864
Thr	Ser	Ala	Lys	Val	Val	Cys	His	Lys	Asp	Ala	Lys	Ile	Arg	Val	Gln	
275							280					285				
gcc	cga	gac	cgc	tac	tat	agt	tca	tcc	tgg	agc	gac	tgg	gca	tct	gtg	912
Ala	Arg	Asp	Arg	Tyr	Tyr	Ser	Ser	Ser	Trp	Ser	Asp	Trp	Ala	Ser	Val	
290							295					300				
tca	tgc	agt	ggt	ggc	ggc	ggc	gga	tct	aga	aac	ttg	cca	acc	cct		960
Ser	Cys	Ser	Gly	Gly	Gly	Gly	Gly	Gly	Ser	Arg	Asn	Leu	Pro	Thr	Pro	
305							310					315			320	
act	cca	tcc	ccg	ggt	atg	ttc	caa	tgt	ttg	aac	cac	tcc	caa	acc	ttg	1008
Thr	Pro	Ser	Pro	Gly	Met	Phe	Gln	Cys	Leu	Asn	His	Ser	Gln	Thr	Leu	

325	330	335	
ttg aga gcc gtc agc aac acg ctt cag aag gcc aga caa act cta gaa Leu Arg Ala Val Ser Asn Thr Leu Gln Lys Ala Arg Gln Thr Leu Glu 340	345	350	1056
tta tat tcc tgc act tcc gaa gag att gat cat gaa gat atc aca aag Leu Tyr Ser Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys 355	360	365	1104
gat aaa acc agc aca gtg gag gcc tgc tta cca ctg gaa tta acc atg Asp Lys Thr Ser Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Met 370	375	380	1152
aat gag agt tgc ctg gct tcc aga gag atc tct ttg ata act aac ggg Asn Glu Ser Cys Leu Ala Ser Arg Glu Ile Ser Leu Ile Thr Asn Gly 385	390	395	1200
agt tgc ctg gcc tct gga aag gcc tct ttt atg acg gtc ctg tgc ctt Ser Cys Leu Ala Ser Gly Lys Ala Ser Phe Met Thr Val Leu Cys Leu 405	410	415	1248
agc agc atc tat gag gac ttg aag atg tac cag atg gaa ttc aag gcc Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr Gln Met Glu Phe Lys Ala 420	425	430	1296
atg aac gca aag ctt tta atg gat ccc aag agg cag atc ttt ctg gat Met Asn Ala Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp 435	440	445	1344
caa aac atg ctg aca gct atc gat gag ctg tta cag gcc ctg aat ttc Gln Asn Met Leu Thr Ala Ile Asp Glu Leu Leu Gln Ala Leu Asn Phe 450	455	460	1392
aac agt gtg act gtg cca cag aaa tcc tcc ctt gaa gag ccg gat ttt Asn Ser Val Thr Val Pro Gln Lys Ser Ser Leu Glu Glu Pro Asp Phe 465	470	475	1440
tat aaa act aaa atc aag ctc tgc ata ctt ctt cat gct ttc aga att Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile 485	490	495	1488
cgt gcg gtg acc atc aat aga atg atg tcc tac ttg aac tct tcc Arg Ala Val Thr Ile Asn Arg Met Met Ser Tyr Leu Asn Ser Ser 500	505	510	1533
<210> 67			
<211> 511			
<212> PRT			
<213> Canis familiaris			
<400> 67			
Ile Trp Glu Leu Glu Lys Asp Val Tyr Val Val Glu Leu Asp Trp His			
1	5	10	15

Pro Asp Ala Pro Gly Glu Met Val Val Leu Thr Cys His Thr Pro Glu
20 25 30

Glu Asp Asp Ile Thr Trp Thr Ser Ala Gln Ser Ser Glu Val Leu Gly
35 40 45

Ser Gly Lys Thr Leu Thr Ile Gln Val Lys Glu Phe Gly Asp Ala Gly
50 55 60

Gln Tyr Thr Cys His Lys Gly Gly Lys Val Leu Ser Arg Ser Leu Leu
65 70 75 80

Leu Ile His Lys Lys Glu Asp Gly Ile Trp Ser Thr Asp Ile Leu Lys
85 90 95

Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe Leu Lys Cys Glu Ala Lys
100 105 110

Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp Leu Thr Ala Ile Ser Thr
115 120 125

Asp Leu Lys Phe Ser Val Lys Ser Ser Arg Gly Phe Ser Asp Pro Gln
130 135 140

Gly Val Thr Cys Gly Ala Val Thr Leu Ser Ala Glu Arg Val Arg Val
145 150 155 160

Asp Asn Arg Asp Tyr Lys Tyr Thr Val Glu Cys Gln Glu Gly Ser
165 170 175

Ala Cys Pro Ser Ala Glu Glu Ser Leu Pro Ile Glu Val Val Val Asp
180 185 190

Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr Thr Ser Ser Phe Phe Ile
195 200 205

Arg Asp Ile Ile Lys Pro Asp Pro Pro Thr Asn Leu Gln Leu Lys Pro
210 215 220

Leu Lys Asn Ser Arg His Val Glu Val Ser Trp Glu Tyr Pro Asp Thr
225 230 235 240

Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr Phe Cys Ile Gln Ala
245 250 255

Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp Arg Leu Cys Val Asp Lys
260 265 270

Thr Ser Ala Lys Val Val Cys His Lys Asp Ala Lys Ile Arg Val Gln
275 280 285

Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp Ser Asp Trp Ala Ser Val
290 295 300

Ser Cys Ser Gly Gly Gly Gly Ser Arg Asn Leu Pro Thr Pro
305 310 315 320

Thr Pro Ser Pro Gly Met Phe Gln Cys Leu Asn His Ser Gln Thr Leu
325 330 335

Leu Arg Ala Val Ser Asn Thr Leu Gln Lys Ala Arg Gln Thr Leu Glu
340 345 350

Leu Tyr Ser Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys
355 360 365

Asp Lys Thr Ser Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Met
370 375 380

Asn Glu Ser Cys Leu Ala Ser Arg Glu Ile Ser Leu Ile Thr Asn Gly
385 390 395 400

Ser Cys Leu Ala Ser Gly Lys Ala Ser Phe Met Thr Val Leu Cys Leu
405 410 415

Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr Gln Met Glu Phe Lys Ala
420 425 430

Met Asn Ala Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp
435 440 445

Gln Asn Met Leu Thr Ala Ile Asp Glu Leu Leu Gln Ala Leu Asn Phe
450 455 460

Asn Ser Val Thr Val Pro Gln Lys Ser Ser Leu Glu Glu Pro Asp Phe

465 470 475 480

Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile
485 490 495

Arg Ala Val Thr Ile Asn Arg Met Met Ser Tyr Leu Asn Ser Ser
500 505 510

<210> 68
<211> 1533
<212> DNA
<213> Canis familiaris

<400> 68
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ctgtggcaca gtcacactgt taaaattcag ggcctgtaac agctcatcga tagctgtcag 180
catgttttga tccagaaaaga tctgcctctt gggatccatt aaaagctttg cgttcatggc 240
cttgaattcc atctggtaca tcttcaagtc ctcatagatg ctgctaaggc acaggaccgt 300
cataaaagag gcctttccag aggccaggca actccgtta gttatcaaag agatctct 360
ggaagccagg caactctcat tcatggtaa ttccagtggt aagcaggcct ccactgtgct 420
ggtttatcc tttgtgatat ctcatgatc aatctttcg gaagtgcagg aatataattc 480
tagagtttgt ctggccttct gaagcgtgtt gctgacggct ctcaacaagg tttgggagtg 540
gttcaaacat tggaacatac ccggggatgg agtaggggtt ggcaagttc tagatccgcc 600
gccaccgcca ccactgcatg acacagatgc ccagtcgctc caggatgaac tatagtagcg 660
gtctcgggct tgcacgcgga tcttggcatc cttgtggcac acgaccttgg ctgaggtctt 720
gtccacgcag agtctatctt tctttctct attgttcttgc ccctgggcct gtatgaaaa 780
tgtcagggag aagtaggaat gtggggtgct ccaggtgtcg gggattccc agctgacctc 840
cacgtgccga gaattttca atggcttcag ctgcagggtt gtgggtgggt ctggtttgat 900
gatgtctctg atgaagaagc tgctggtgta gtttcatac ttgagcttgt gaatagcatc 960
caccacgacc tcgatggta ggctctcctc ggcagagggg caggcactgc cctcctgaca 1020
ctccactgtg tacttcttat aatccctgtt gtccactctg accctctctg ctgaaaagtgt 1080
cactgctcca catgtcaccc cttgggggtc agagaagcct ctgctacttt tgacactgaa 1140
tttcaaatca gtactgattt ccgtcagcca ccagcatgtg aaacgtccag aataattctt 1200

tgcctcacat ttcagaaaga tcattttttt ggatttttc tgttcctta agatatcgt	1260
ggaccaaatt ccatcttctt ttttgtaat caacaggagt gagcggctca gaaccttgcc	1320
tccttatgg caggtatact gcccagcatc tccaaattct ttgacttggta tggtcagagt	1380
tttaccagaa cctaggactt cactgctctg cgctgaggc caagtgtatgt catcttcttc	1440
aggggtatgg caggtgagga ccaccatttc tccggggca tcagggtgcc agtccaactc	1500
tacaacataa acatcttctt ccagttccca tat	1533

<210> 69
<211> 30
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<220>
<223> Synthetic Primer

<400> 69 gc当地 gctcg aaattaaccc tcactaaagg	30
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<210> 70
<211> 28
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 70 cgacggccag tgaattgtaa tacgactc	28
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<210> 71
<211> 31
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 71 agtatgaag gcctgaaatc agattacttt g	31
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<210> 72
<211> 32
<212> DNA
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<220>
<223> Synthetic Primer

<400> 72	atggcctgga acacttctct gaaagaatat ga	32
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<211> 30		
<212> DNA		
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<211> 33		
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<210> 76		
<211> 37		
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<210> 77		
<211> 28		
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atggccgaca aggtcctgaa ggagaaga		28
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<210> 80		
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<210> 81		
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cgccctctaga cctcaattgc caggaaagag atagaagta		39
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ctgcagtggc ggcgggtggcg gcggatctag aaacttgcca acccctactc catccccggg		60
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cccggggatg gagtaggggt tggcaagttt ctagatccgc cgccaccgcc accactgcag		60
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<211> 19	
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<210> 90	
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<210> 91	
<211> 39	
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<210> 93		
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gcggccgctc gagtaggaa gagttcaagt aggacatcat tctattgatg g		51
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<223> Synthetic Primer		
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<210> 98		
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<223> Synthetic Primer		
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ggtattccca gctgaccc		19
<210> 99		
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<212> DNA		
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<211> 29		
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<210> 101		
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<212> DNA
<213> *Felis catus*

<220>
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<222> (1) .. (561)

<400> 101

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ggg atg ttc cag tgc ctc aac cac tcc caa acc ctg ctg cga gcc atc      48
Gly Met Phe Gln Cys Leu Asn His Ser Gln Thr Leu Leu Arg Ala Ile
1          5            10           15

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agc aac acg ctt cag aag gcc aga caa act cta gaa ttt tac tcc tgc 96
Ser Asn Thr Leu Gln Lys Ala Arg Gln Thr Leu Glu Phe Tyr Ser Cys
          20           25           30

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act tcc gaa gag att gat cat gaa gat atc aca aaa gat aaa acc agc 144
 Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp Lys Thr Ser
 35 40 45

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aca gtg gag gcc tgc tta cca ctg gaa tta acc atg aat gag agt tgc      192
Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Met Asn Glu Ser Cys
      50           55           60

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ctg gct tcc aga gag atc tct ctg ata act aat ggg agt tgc ctg gcc      240
Leu Ala Ser Arg Glu Ile Ser Leu Ile Thr Asn Gly Ser Cys Leu Ala
65          .    70           .    75           .    80

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tcc aga aag acc tct ttt atg acg acc ctg tgc ctt agc agt atc tat	288
Ser Arg Lys Thr Ser Phe Met Thr Thr Leu Cys Leu Ser Ser Ile Tyr	
85 90 95	

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gag gac ttg aag atg tac cag gtg gag ttc aag gcc atg aat gca aag      336
Glu Asp Leu Lys Met Tyr Gln Val Glu Phe Lys Ala Met Asn Ala Lys
          100           105           110

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ctg tta atg gat cct aaa agg cag atc ttt ctg gat caa aac atg ctg 384
 Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln Asn Met Leu
 115 120 125

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aca gct att gag ctg tta cag gcc ctg aat gtc aac agt gtg act      432
Thr Ala Ile Asp Glu Leu Leu Gln Ala Leu Asn Val Asn Ser Val Thr
130          135          140

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atc aag ctc tgc ata ctt ctt cat gct ttc aga att cgt gca gtg acc 528
Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg Ala Val Thr
165 170 175

atc aat aga atg atg agc tat ctg aat gct tcc 561
Ile Asn Arg Met Met Ser Tyr Leu Asn Ala Ser
180 185

<210> 102
<211> 187
<212> PRT
<213> Felis catus

<400> 102

Gly Met Phe Gln Cys Leu Asn His Ser Gln Thr Leu Leu Arg Ala Ile
1 5 10 15

Ser Asn Thr Leu Gln Lys Ala Arg Gln Thr Leu Glu Phe Tyr Ser Cys
20 25 30

Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp Lys Thr Ser
35 40 45

Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Met Asn Glu Ser Cys
50 55 60

Leu Ala Ser Arg Glu Ile Ser Leu Ile Thr Asn Gly Ser Cys Leu Ala
65 70 75 80

Ser Arg Lys Thr Ser Phe Met Thr Thr Leu Cys Leu Ser Ser Ile Tyr
85 90 95

Glu Asp Leu Lys Met Tyr Gln Val Glu Phe Lys Ala Met Asn Ala Lys
100 105 110

Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln Asn Met Leu
115 120 125

Thr Ala Ile Asp Glu Leu Leu Gln Ala Leu Asn Val Asn Ser Val Thr
130 135 140

Val Pro Gln Asn Ser Ser Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys
145 150 155 160

Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg Ala Val Thr
165 170 175

Ile Asn Arg Met Met Ser Tyr Leu Asn Ala Ser
180 185

<210> 103

<211> 561
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 <213> Felis catus

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 ctgtggcaca gtcacactgt tgacattcag ggcctgtaac agctcatcaa tagctgtcag 180
 catgtttga tccagaaaaga tctgcctttt aggatccatt aacagcttg cattcatggc 240
 cttgaactcc acctggtaca tcttcaagtc ctcataagata ctgctaaggc acagggtcgt 300
 cataaaagag gtctttctgg aggccaggca actcccatta gttatcagag agatctct 360
 ggaagccagg caactctcat tcatggtaa ttccagtggt aagcaggcct ccactgtgct 420
 ggtttatct tttgtgatat cttcatgatc aatctttcg gaagtgcagg agtaaaattc 480
 tagagttgt ctggccttct gaagcgtgtt gctgatggct cgacgcaggg tttggagtg 540
 gttgaggcac tggAACATCC C 561

<210> 104
 <211> 1455
 <212> DNA
 <213> Canis familiaris

<220>
 <221> CDS
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 gccaattata aaaatgtgac cccccgggtc ggcctccac cgccgcctc ccctgccg 180
 tccgcagtcc gcgtccagcg cccgcgggg tccacgcagc gcccgcctag C atg tgc 237
 Met Cys
 1

ccg ccg cgc ggc ctc ctc ctt gtg acc atc ctg gtc ctg cta agc cac	285
Pro Pro Arg Gly Leu Leu Val Thr Ile Leu Val Leu Leu Ser His	
5	10
15	

ctg gac cac ctt act tgg gcc agg agc ctc ccc aca gcc tca ccg agc 333
 Leu Asp His Leu Thr Trp Ala Arg Ser Leu Pro Thr Ala Ser Pro Ser
 20 25 30

cca gga ata ttc cag tgc ctc aac cac tcc caa aac ctg ctg aga gcc	381
Pro Gly Ile Phe Gln Cys Leu Asn His Ser Gln Asn Leu Leu Arg Ala	

35	40	45	50	
gtc agc aac acg ctt cag aag gcc aga caa act cta gaa tta tat tcc Val Ser Asn Thr Leu Gln Lys Ala Arg Gln Thr Leu Glu Leu Tyr Ser				429
55	60	65		
tgc act tcc gaa gag att gat cat gaa gat atc aca aag gat aaa acc Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp Lys Thr				477
70	75	80		
agc aca gtg gag gcc tgc tta cca ctg gaa tta acc atg aat gag agt Ser Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Met Asn Glu Ser				525
85	90	95		
tgc ctg gct tcc aga gag atc tct ttg ata act aac ggg agt tgc ctg Cys Leu Ala Ser Arg Glu Ile Ser Leu Ile Thr Asn Gly Ser Cys Leu				573
100	105	110		
gcc tct gga aag gcc tct ttt atg acg gtc ctg tgc ctt agc agc atc Ala Ser Gly Lys Ala Ser Phe Met Thr Val Leu Cys Leu Ser Ser Ile				621
115	120	125	130	
tat gag gac ttg aag atg tac cag atg gaa ttc aag gcc atg aac gca Tyr Glu Asp Leu Lys Met Tyr Gln Met Glu Phe Lys Ala Met Asn Ala				669
135	140	145		
aag ctt tta atg gat ccc aag agg cag atc ttt ctg gat caa aac atg Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln Asn Met				717
150	155	160		
ctg aca gct atc gat gag ctg tta cag gcc ctg aat ttc aac agt gtg Leu Thr Ala Ile Asp Glu Leu Leu Gln Ala Leu Asn Phe Asn Ser Val				765
165	170	175		
act gtg cca cag aaa tcc tcc ctt gaa gag ccg gat ttt tat aaa act Thr Val Pro Gln Lys Ser Ser Leu Glu Glu Pro Asp Phe Tyr Lys Thr				813
180	185	190		
aaa atc aag ctc tgc ata ctt ctt cat gct ttc aga att cgt gcg gtg Lys Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg Ala Val				861
195	200	205	210	
acc atc gat aga atg atg agt tat ctg aat tct tcc taaaaagctg Thr Ile Asp Arg Met Met Ser Tyr Leu Asn Ser Ser				907
215	220			
aggctctct cgactttaaa gtcattccta taaaaatgtg aacccaaaag aattttcat				967
aagatagggg ttaagaacca gggagggggt ggcttgacct ggtcctactt aagcttagtac				1027
gataattctc atgcttgttt acattagttg ccactcaa at tttgaaagat gtgactgtta				1087
tatccccacac gatgcctttg accaagtata tttcacattt actatggata agttaagtgt				1147
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taatagaaga gcaagacttt ataagctatt tctgtaccaa actgtttgta gaaacaaaca				1267

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gaatttaattt atatttatTT atgttatatt tattaaagta tttattatca agtggatttg 1387
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aaaaaaaaa 1455

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<211> 222
<212> PRT
<213> Canis familiaris

<400> 105

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35 40 45

Arg Ala Val Ser Asn Thr Leu Gln Lys Ala Arg Gln Thr Leu Glu Leu
50 55 60

Tyr Ser Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp
65 70 75 80

Lys Thr Ser Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Met Asn
85 90 95

Glu Ser Cys Leu Ala Ser Arg Glu Ile Ser Leu Ile Thr Asn Gly Ser
100 105 110

Cys Leu Ala Ser Gly Lys Ala Ser Phe Met Thr Val Leu Cys Leu Ser
115 120 125

Ser Ile Tyr Glu Asp Leu Lys Met Tyr Gln Met Glu Phe Lys Ala Met
130 135 140

Asn Ala Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln
145 150 155 160

Asn Met Leu Thr Ala Ile Asp Glu Leu Leu Gln Ala Leu Asn Phe Asn
165 170 175

Ser Val Thr Val Pro Gln Lys Ser Ser Leu Glu Glu Pro Asp Phe Tyr
180 185 190

Lys Thr Lys Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg
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Ala Val Thr Ile Asp Arg Met Met Ser Tyr Leu Asn Ser Ser
210 215 220

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<211> 1455
<212> DNA
<213> Canis familiaris

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<213> Canis familiaris

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	cccagggAAC	cttgcagcct	ggccagaAGC	aAG	ATG	CAT	CCT	CAG	TTG	GTC	174	
					Met	His	Pro	Gln	Gln	Leu	Val	
					1					5		
	atc tcc tgg	ttt tcc ctc	gtt ttg ctg	gcg tct	ccc ctc	atg	gcc	ata				222
	Ile Ser Trp	Phe Ser Leu	Val Leu Leu	Ala Ser Pro	Leu Met Ala	Ile						
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	tgg gaa ctg	gag aaa gat	gtt tat	gtt gta	gag ttg	gac tgg	cac cct					270
	Trp Glu Leu	Glu Lys Asp	Val Tyr Val	Val Glu Leu	Asp Trp His	Asp	Trp His	Pro				
	25	30	35									
	gat gcc ccc	gga gaa atg	gtg gtc	ctc acc	tgc cat	acc cct	gaa gaa					318
	Asp Ala Pro	Gly Glu Met	Val Val Leu	Thr Cys His	Thr Pro	Glu Glu						
	40	45	50	55								
	gat gac atc	act tgg acc	tca gcg	cag agc	agt gaa	gtc cta	ggt tct					366
	Asp Asp Ile	Thr Trp Thr	Ser Ala Gln	Ser Ser	Glu Val	Leu Gly	Ser					
	60	65	70									
	ggt aaa act	ctg acc atc	caa gtc	aaa gaa	ttt gga	gat gct	ggc cag					414
	Gly Lys Thr	Leu Thr Ile	Gln Val Lys	Glu Phe	Gly Asp	Ala Gly	Gln					
	75	80	85									
	tat acc tgc	cat aaa gga	ggc aag	gtt ctg	agc cgc	tca ctc	ctg ttg					462
	Tyr Thr Cys	His Lys Gly	Gly Lys Val	Leu Ser Arg	Ser Leu	Leu	Leu					

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cag aaa gaa tcc aaa aat aag atc ttt ctg aaa tgt gag gca aag aat Gln Lys Glu Ser Lys Asn Lys Ile Phe Leu Lys Cys Glu Ala Lys Asn 120	125	130	558
tat tct gga cgt ttc aca tgc tgg tgg ctg acg gca atc agt act gat Tyr Ser Gly Arg Phe Thr Cys Trp Trp Leu Thr Ala Ile Ser Thr Asp 140	145	150	606
ttg aaa ttc agt gtc aaa agt agc aga ggc ttc tct gac ccc caa ggg Leu Lys Phe Ser Val Lys Ser Ser Arg Gly Phe Ser Asp Pro Gln Gly 155	160	165	654
gtg aca tgt gga gca gtg aca ctt tca gca gag agg gtc aga gtg gac Val Thr Cys Gly Ala Val Thr Leu Ser Ala Glu Arg Val Arg Val Asp 170	175	180	702
aac agg gat tat aag aag tac aca gtg gag tgt cag gag ggc agt gcc Asn Arg Asp Tyr Lys Lys Tyr Thr Val Glu Cys Gln Glu Gly Ser Ala 185	190	195	750
tgc ccc tct gcc gag gag agc cta ccc atc gag gtc gtg gtg gat gct Cys Pro Ser Ala Glu Glu Ser Leu Pro Ile Glu Val Val Val Asp Ala 200	205	210	798
att cac aag ctc aag tat gaa aac tac acc agc agc ttc ttc atc aga Ile His Leu Lys Tyr Glu Asn Tyr Thr Ser Ser Phe Phe Ile Arg 220	225	230	846
gac atc atc aaa cca gac cca ccc aca aac ctg cag ctg aag cca ttg Asp Ile Ile Lys Pro Asp Pro Pro Thr Asn Leu Gln Leu Lys Pro Leu 235	240	245	894
aaa aat tct cgg cac gtg gag gtc agc tgg gaa tac ccc gac acc tgg Lys Asn Ser Arg His Val Glu Val Ser Trp Glu Tyr Pro Asp Thr Trp 250	255	260	942
agc acc cca cat tcc tac ttc tcc ctg aca ttt tgc ata cag gcc cag Ser Thr Pro His Ser Tyr Phe Ser Leu Thr Phe Cys Ile Gln Ala Gln 265	270	275	990
ggc aag aac aat aga gaa aag aaa gat aga ctc tgc gtg gac aag acc Gly Lys Asn Asn Arg Glu Lys Lys Asp Arg Leu Cys Val Asp Lys Thr 280	285	290	1038
tca gcc aag gtc gtg tgc cac aag gat gcc aag atc cgc gtg caa gcc Ser Ala Lys Val Val Cys His Lys Asp Ala Lys Ile Arg Val Gln Ala 300	305	310	1086
cga gac cgc tac tat agt tca tcc tgg agc gac tgg gca tct gtg tcc Arg Asp Arg Tyr Tyr Ser Ser Trp Ser Asp Trp Ala Ser Val Ser 315	320	325	1134

tgc agt taggttccac ccccaggatg aatcttgag ggaaagtgg a agatattatg Cys Ser	1190
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<213> Canis familiaris

<400> 108

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Val Glu Leu Asp Trp His Pro Asp Ala Pro Gly Glu Met Val Val Leu
35 40 45

Thr Cys His Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser Ala Gln
50 55 60

Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys
65 70 75 80

Glu Phe Gly Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Lys Val
85 90 95

Leu Ser Arg Ser Leu Leu Ile His Lys Lys Glu Asp Gly Ile Trp
100 105 110

Ser Thr Asp Ile Leu Lys Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe
115 120 125

Leu Lys Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp
130 135 140

Leu Thr Ala Ile Ser Thr Asp Leu Lys Phe Ser Val Lys Ser Ser Arg
145 150 155 160

Gly Phe Ser Asp Pro Gln Gly Val Thr Cys Gly Ala Val Thr Leu Ser
165 170 175

Ala Glu Arg Val Arg Val Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val
180 185 190

Glu Cys Gln Glu Gly Ser Ala Cys Pro Ser Ala Glu Glu Ser Leu Pro
195 200 205

Ile Glu Val Val Val Asp Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr
210 215 220

Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Thr
225 230 235 240

Asn Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg His Val Glu Val Ser
245 250 255

Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu

260 265 270

Thr Phe Cys Ile Gln Ala Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp
275 280 285

Arg Leu Cys Val Asp Lys Thr Ser Ala Lys Val Val Cys His Lys Asp
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aggcatccaa aaactaaact tgctaaaaaa tgcaagtggc cctgaattgc tttatcaaca 540
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 <213> Artificial

<220>
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<400> 110

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<210> 111
<211> 10
<212> PRT
<213> *Felis catus*

<400> 111

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